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(71) Applicant (for all designated States except US): **COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH [IN/IN]**; Rafi Marg, New Delhi 110 001 (IN).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **VERMA, Sunil, Kumar [IN/IN]**; Centre for Cellular and Molecular Biology, Hyderabad 500 007 (IN). **SINGH, Lalji [IN/IN]**; Centre for Cellular and Molecular Biology, Hyderabad 500 007 (IN).

(74) Agent: **GABRIEL, Devadoss, Calab**; Kumaran & Sagar, 84-C, C6 Lane, (Off Central Avenue), Sainik Farms, New Delhi 110 062 (IN).

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(54) Title: UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION

(57) Abstract: The invention provides novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin and a method for identification of the specific animal from a given biological sample.

## UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION

### TECHNICAL FIELD

The invention relates to the identification of novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) 5 and reveal the identity of the biological material of any unknown animal origin at species and sub-species sources. The invention also provides a method for the identification of fragments on mitochondrial cytochrome b gene in biological material of unknown origin.

### BACKGROUND ART

A large number of studies in evolutionary biology utilize phylogenetic information 10 obtained from mitochondrial cytochrome b gene. It has been identified a potent molecule to distinguish the phylogenetic depth of different lineages to family, genus and species in molecular taxonomy<sup>1-66</sup>. A vast database of the sequences of cytochrome b gene of different animal species has accumulated in public databases such as GenBank, NCBI (http://www.ncbi.nlm.nih.gov) etc. We have utilized this capacity of cytochrome b gene in 15 establishing the identity of the origin of animal parts and product to its family, genus and species sources. The technique developed is based on a pair of universal primer that can amplify a small fragment of cytochrome b gene from a vast range of animal species.

Establishing identity of confiscated animal parts and products is a great challenge to law enforcement agencies because none of the methods available till date is too efficient to 20 reveal the identity of animal remains beyond a reasonable doubt. Morphological markers, described for certain species allow the identification of complete specimen of animals<sup>67</sup>. However, a complete specimen is confiscated very rarely by the investigation agencies; therefore, these marker are not practical in wildlife forensics. The biochemical traits such 25 as the bile characteristics<sup>68</sup> blood haem analysis<sup>69,70</sup> etc. have also been employed in wildlife forensic for identification of individual species. The difficulty of these markers are that these markers are limited in number and are rarely found in their natural forms in which these were originally described as the characteristic of a particular species.

The molecular approaches such as micro-satellite based identification<sup>71</sup>, Restriction 30 fragment length polymorphism analysis of mitochondrial genes or PCR based species specific STS markers require the prior information of the species to establish the identity<sup>72,73</sup>. These methods also need a significant amount of DNA material to be analysed. We may not have the prior information about the species origin of confiscated animal parts and product in forensics. therefore, these methods are not really useful and

practical in wildlife identification. The technique invented by us is universal, therefore does not require any background information to establish the identity of any unknown confiscated remains at family, genus and species sources. Being a PCR based procedure it can be applied with trace amount of any biological material. Because the amplicon length 5 is small (472 bp); therefore, it can work perfectly with the mutilated remains, which are commonly seized by the crime investigation agencies. It does not require the large amount of genetic material i.e. DNA to be analyzed to establish the identity, hence, can detect a minute amount of adulteration in food products. The procedure described is simple and very fast. Due to the said advantages, the procedure invented by us is most suited for 10 forensic wildlife identification.

#### **OBJECTS OF THE INVENTION**

The main object of the invention is to identify a fragment on mitochondrial cytochrome b gene capable of significantly discriminating among various evolutionary lineages of 15 different animal species.

Another object is to identify a fragment on mitochondrial cytochrome b gene which is flanked by the highly conserved sequences at a vast range of animal species.

Yet another object is to detect a fragment on mitochondrial cytochrome b gene which is polymorphic inter-specifically, but monomorphic at intra species sources.

20 Still another object is to develop the universal primers to amplify the fragment on mitochondrial cytochrome b gene using polymerase chain reaction.

Another object is to develop a PCR protocol that works universally with DNA template of any unknown origin (i.e. all the animal species).

25 Yet another object is to provide a universal method for identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.

Still another object is to provide a universal method of animal identification to establish the crime with the criminal beyond a reasonably doubt.

30 Another object is provide a universal method to establish the identity of biological materials such as skin, horns etc confiscated from animal poachers, if it is that of an endangered species.

35 Yet another object is to provide a universal method for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation to the wildlife resources could be controlled.

Still another object is to provide a universal technique to have an idea of the geographical location of the commitment of wildlife crime based on the haplotype of poached animal – identified by the universal primer invented.

Another object is to provide a universal technique of animal identification to detect the 5 adulteration of animal meat/products in vegetarian food product for the purpose of food fortification, by the food fortification agencies.

Yet another object is to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as 10 if criminals have wontedly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic scientists with human blood.

Another object is to invent and authenticate a universal technique that can be converted to a (a) 'MOLECUALR KIT' and (b) 'DNA CHIPS' based application to meet the requirements of above objectives.

## 15 **SUMMARY OF THE INVENTION**

Accordingly, the invention provides novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin

## **DETAILED DESCRIPTION OF THE INVENTION**

20 Keeping in view the above objectives, the cytochrome b gene sequences (1140 bp) of 221 distantly related animal species (listed in Table 1) representing various families were obtained from public database NCBI (<http://www.ncbi.nlm.nih.gov>). These sequences were aligned using the software *Clustal X(1.8)*(NCBI, USA) and a fragment (of 472 bp, alignment shown in Table 2) of gene was identified which had all the features mentioned 25 above under column 1, 2 and 3 of sub-heading 'Objectives of invention'. As for the identity of this fragment we would like to mention that it includes the nucleotides between 398 to 869 in *Antilope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions (marked as star (\*)) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, giving rise to 30 their unique molecular signature. These molecular signatures are characteristic of its species and form the basis of revealing the identity of the biological material of an unknown animal origin by the procedure invented by us. Considering *Antilope cervicapra* as a representative species, the sequence of this fragment is mentioned herewith:  
Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*:

"taccatgaggacaatactttttagggcaacagtcatcaccaatcccttcagcaatcccatacatcggtacaaaccttagtaga  
atgaatctgaggagggtctcagtagataaagcaaccctaccgattttgccttccactttatcctccatttatcattgcagccct  
accatagtacacacctactgttctccacgaaacaggatccaacaacccacaggaatctcatcagacgcagacaaaattccattccac  
ccctactacactatcaaagatatcctaggagctactattaatttaaccctatgcctctagtcatttcaccggacctgctggag  
5 acccagacaactatacaccagcaaaccactaatacacccccacatatcaagcccgaatgatacttcctattgcatacgcaatcc  
ccgatcaattctaacaacttaggagg".

A pair of universal primer was designed to amplify this fragment in polymerase chain

reaction (PCR). These primers were named as 'mcb398' and 'mcb869' because of its property to amplify a region of mitochondrial cytochrome b gene between nucleotides 398

10 to 869 of *Antilope cervicapra*, a representative animal species for this invention. We took

this animal species as representative species because the idea of developing such a novel primers came in the mind of inventors while they were working on the genome of this animal in Centre for Cellular and Molecular Biology, Hyderabad, India. These primers work universally because its 3' end are highly conserved amongst a vast range of animal

15 species (shown in Table 2). As mentioned above, the DNA fragment (sequence of which is shown above) targeted by these primers is highly polymorphic inter-specifically; however,

it is monomorphic among the individual of same species (Tables 6, 7a, 7b, 7c, 7d and 8, respectively). These unique features of the targeted region enable these primers to generate the molecular signatures of an individual species; thereby, enabling them to differentiate

20 amongst the animals of different species (see in Figure 1c). The variation within the fragment amplified by these primers increase with increasing distances of evolutionary

lineages of two animals (Table 8). These unique features of the fragment amplified by the universal primers 'mcb398' and 'mcb869' invented by the applicants fulfill the objectives

of invention.

25 Thus, the primers invented by us can generate the molecular signature from any biological material of unknown animal origin, which actually is the characteristic of its family, genus and more precisely, the species. When these signatures are compared *in-silico* with the

signatures already available in public databases (viz., GenBank, NCBI database etc) using 'BLAST software'<sup>73</sup>, it indicates identity of the family, genus or species of the analyzed

30 material, which in turn is confirmed practically by comparing with the reference animals of

the revealed family, genus or species, by including them in the further analysis by the

primers 'mcb398' and 'mcb869'. The complete procedure involved in the analyses (the word, 'analyses' should be understood with the stepwise procedure to establish the identity

of the biological remain of any unknown animal origin for the aims mentioned in columns

1-13 under sub-heading ‘Objectives of invention’) is briefed under ‘Examples 5 and 6, respectively, as well as illustrated in Figures 1a, 1b and 1c, respectively.

#### BRIEF DESCRIPTION OF DRAWING AND TABLES

**Figure 1a.** Illustration of the step-wise procedure involved in *analyses*. The unknown biological material i.e. ‘adil.flesh’ refers to the confiscated skin mentioned in ‘Example 6’. The arrow marks indicate the stepwise procedure involved. The brief description of Figure 1a is as follows:

The biological material i.e. the confiscated skin ‘adil.flesh’ was subjected to DNA isolation using the standard procedures<sup>74</sup>. The DNA obtained was amplified using the primers ‘mcb398’ and ‘mcb869’ in PCR, fractionated in 2% (w/v) agarose gel, visualized and photographed under UV light using Gel Documentation System (Syngene, USA). The lane ‘M’ shown in the photograph represents the molecular weight marker (Marker XIII, Boehringer mannheim). Lane 1 shows the PCR amplicon (472 bp) obtained from ‘adil.flesh’ using primers ‘mcb398’ and ‘mcb869’. The PCR amplicon obtained were sequenced at both the strand using “ABI Prism 3700 DNA Analyzes, PE-Applied Bio-systems). The chromatogram shows the sequences (about 80 bp long, i.e. between 150-230 bp of sequence (328 bp), revealed from the PCR product of 472 bp length) obtained from ‘adil.flesh’.

**Figure 1b.** Illustrates the further steps involved in *analyses*. The sequence (328 bp) revealed from ‘adil.flesh’ was subjected to homology search in *nr* (i.e. non-redundant) database of National Centre for Biological Information (NCBI), USA. The sequences producing significant alignments are shown along with its bits score and E values. It indicates the extent of homology amongst the sequence enquired (i.e. the 328 bp sequence from adil.flesh) and the sequences registered in *nr* database of NCBI. BLAST analysis revealed the highest homology of the sequence revealed from ‘adil.flesh’ with the sequence of *Panthera pardus* (gene bank registration number ‘AY005809’), indicating the identity of adil.flesh as that of a leopard (*Panthera pardus*) origin. Figure 1b further illustrates the multiple alignments of the sequences obtained from reference animals (listed in Table 5) along with the sequence obtained from ‘adil.flesh’. The sequences of ‘adil.flesh’ is similar to the sequences of ‘gz1L’ further confirming the identity of the source of confiscated remain ‘adil.flesh’ as that of a *Panthera pardus* origin.

**Figure 1c** illustrates the NJ-tree (Neighbor Joining tree) constructed using CLUSTAL X (1.8) from the sequences revealed from ‘adil.flesh’ and reference animals listed in Table 5.

The animals belonging to similar species cluster together; however, the animals of different species group in different clusters. The confiscated material under investigation (i.e. 'adil.flesh') clusters with 'gz1L' (i.e. the known normal leopard '*Panthera pardus*') indicating the identity of the species of 'adil.flesh' as that of a *Panthera pardus* source.

5 **Figure 2** shows the Agarose gel electrophorogram showing the PCR amplicons (472 bp) obtained from the reference animals of family felidae listed in Table 5, using universal primers 'mcb398 and 'mcb869'. Description of different lanes is as follows:

Lanes 1-21: The PCR profiles of the animals 1-21, respectively, listed in Table 5.

Lane 22: The PCR profiles of DNA isolated from confiscated skin of unknown animal

10 origin 'i.e. adil.flesh'

Lane 23: Negative control (no DNA)

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

**Figure 3.** Shows PCR amplicons obtained from animals listed in Table 9. The primers used in PCR are 'AFF' and 'AFR'. The description of different lanes shown is as follows:

15 Lane 1-4: The PCR profiles of animals 1-4, respectively, listed in Table 9, showing amplicons of 354 bp.

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

**Figure 4.** Shows PCR amplicons obtained from animals listed in Table 12. This experiment demonstrates the universal nature of our primers among a vast range of animal

20 species. Description of different lanes shown is as follows:

Lanes 1-23: The PCR profiles of the animals 1-23, respectively, listed in Table 12. The PCR product of 472 bp is amplified universally from all the animal species analyzed.

Lane 24: Negative control (no DNA)

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

25 **Table 1.** List of 221 animal species used for *In-silico* analysis to design the universal primers 'mcb398' and 'mcb869'. Table also demonstrate the 'P,S scores' of 'mcb398' and 'mcb869' for different templates. The descriptions of various symbols used in this table are as follows:

Symbol (#) refers to Number

30 Symbol (\*) refers to the animal species which is either protected species (listed in Wildlife (Protection) Act , 1972 (Central Act NO 53 of 1972), or an endangered/rare animal species

Symbol (<sup>§</sup>P,S/F) refers to Probability of match and Stability of match of primer 'mcb398' with different templates (i.e. the cytochrome b gene from different species origin). A higher P, S score refers to the higher probabilities of significant amplification of specific

template by the primer. It is calculated by *Amplify* (1.2) software.

Symbol ("P,S/R) refers to Probability of match and Stability of match of primer 'mcb869' with different templates. A higher P,S score refers to the higher probabilities of significant amplification of specific template by the primer. It is calculated by *Amplify* (1.2) software.

5      **Table 2.** Multiple sequence alignment of 472 bp fragment of mitochondrial cytochrome b gene (identified by inventors to fulfill the requirements of column 1, 2 and 3 mention under sub-heading 'Objectives of invention') of 221 animal species listed in Table 1. Alignments also show the binding sites for universal primers 'mcb398' and 'mcb869'. The symbol (\*) refers to the nucleotide bases which are conserved amongst 221 animal species  
10     listed in Table 1). The alignments have been done using software *CLUSTAL X* (1.8). The nucleotide positions that are unmarked are variable amongst 221 animal species analyzed. These variable sites together constitute the molecular signature of an individual species, giving rise to molecular basis of species identification by our primers.

15     **Table 3.** Results of the blast analysis of the sequence revealed from 'adil.flesh' in '*mito*' database of NCBI. It shows the most significant alignment of cytochrome b sequence (328 bp) revealed from confiscated skin piece 'adil.flesh' with *felis catus* cytochrome b gene sequence (genbank registration number NC\_001700.1, bits score 365, E value, e-101) registered in NCBI database (bits score 365 and E value e-101). It gives an indication that the species of analyzed material belongs to family felidae. It also fulfills the requirements  
20     of column 6 mention above under sub-heading 'Objectives of invention'.

25     **Table 4.** Results of the blast analysis of the sequence revealed from 'adil.flesh' in '*nr*' database of NCBI. It shows the most significant alignment of cytochrome b sequence (328 bp) revealed from confiscated skin piece 'adil.flesh' with *Panthera pardus* cytochrome b gene sequence (genbank registration number AY005809, bits score 603, E value, e-170) registered in NCBI database. It gives an indication that the species of analyzed material belongs to *Panthera pardus* origin. It also fulfills the requirements of column 6 mention above under sub-heading 'Objectives of invention'.

30     **Table 5.** Reference animal belonging to family felidae selected for comparison with 'adil.flesh' to confirm the findings of BLAST analysis results of which are mentioned in Table 3 and 4, respectively. The animals listed in SN. 1-21 represent different species of family felidae. SN. 22 and 23 are primate species taken for out-group comparisons.

**Table 6** Multiple sequence alignments of cytochrome b sequences (328 bp) revealed from 'adil.flesh' and reference animals listed in Table 5. The positions that have a common nucleotide in all the animal species under investigation are shown with a star (\*) mark;

however, the positions that are variable in any of the animals under investigation are unmarked. The nucleotides at these positions constitute the molecular signature of an individual species, which are unique and highly specific for its species. These signatures are the molecular basis of identification of individual animal species using our primers 5 'mcb398' and 'mcb869'.

**Table 7** (Tables 7a, 7b, 7c and 7d). The comparison of the molecular signatures of different animal species investigated along with 'adil.flesh', the confiscated skin of unknown animal origin. This table demonstrates the variable positions (i.e. the positions which are not marked with star (\*) symbol in Table 6), amongst the 328 bp fragment 10 revealed from the animals listed in Table 5. The dot (.) mark represents the presence of the similar nucleotide as listed in lane 1 i.e. the sequence from "adil.flesh" at that position. It demonstrates that the signatures of each species are unique and specific to its species. The molecular signatures of 'adil.flesh' are comparable (except for position 37 which has a transition from 'T' to 'C') to the molecular signature of 'gz1L' i.e. the known leopard 15 'Panthera pardus' source, indicating the identity of the source of confiscated skin 'adil.flesh' as that of a leopard 'Panthera pardus' source. The nucleotide variations (at the positions 153, 198, 223, 264, among the known leopards, (i.e. gz1L, gz2L, and gz3L, respectively)), give an idea about the geographical habitat of each animals. Various studies referring to molecular evolution of different animal species support this hypothesis<sup>75</sup>; 20 however, it could further be confirmed by taking the reference animals from different geographical areas and analyzing by our primers 'mcb 398' and 'mcb869'. If we could generate the database of different haplotypes (i.e. habitat specific molecular signatures) of the animal species, it would also enable our primers to reveal the geographical location of the commitment of wildlife crime.

25 **Table 8.** Percent similarity matrix calculated by pair-vise comparisons of nucleotide sequences aligned (illustrated in Table 6). The cytochrome b gene sequence of DNA isolated from confiscated material had maximum similarity (99.7% and 98.2%, with the lineages of animals 'gz2L' and 'gz3L', respectively) with the sequences obtained from known normal leopard source, indicating its identity as that of a leopard origin. The 30 similarity matrix has been calculated using the software *PHYLIP* (3.5).

**Table 9.** Animals selected for validation of minimum P,S score for efficient amplification of cytochrome b gene of different origin by the primers 'mcb398' and 'mcb869'. P,S score of primers 'AFF' and 'AFR' for these animals are shown.

**Table 10.** BLAST analysis of primers 'mcb398' in *nr* database of NCBI . It demonstrates

that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer

**Table 11.** BLAST analysis of primers 'mcb869' in *nr* database of NCBI. It demonstrates

5 that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer.

**Table 12.** Other animal belonging to distantly related animal species, investigated to

10 confirm the universal nature of primers 'mcb398' and 'mcb869'. Gel photograph showing the PCR amplicons from these animals are shown in Figure 4.

The mitochondrial cytochrome b gene has very widely been used in molecular taxonomic studies. It has immense capabilities to reveal different evolutionary lineages of animals in family, genus and species specific manner. It has also been used to classify the population

15 of a particular species according to its demographic distributions<sup>75</sup>. The vast database of cytochrome b sequences of different animal species has accumulated in public databases such as Genbank and NCBI<sup>1-65</sup>. We have explored these unique characteristics of cytochrome b gene to establish the identity of confiscated remains of any unknown animal by inventing a pair of novel primers, 'mcb398' and 'mcb869', that can amplify a small 20 fragment (472 bp) of cytochrome b gene of wide range of animal species in universal manner. These primers work universally because its 3' ends target within a highly conserved region.

The fragment of cytochrome b gene identified had all the features mentioned in columns 1,

2 and 3 listed under sub-heading 'Objective of invention'. We identified this fragment by

25 aligning the cytochrome b gene sequences (1140 bp) of 221 different animal species listed in Table 1. These sequences are publicly available in NCBI DNA databases. These sequences were aligned using the software CLUSTAL X (1.8). As mentioned before, the

472 bp fragment of cytochrome b gene identified by us to have the features mentioned in columns 1, 2 and 3 listed under sub-heading 'Objective of invention' includes the

30 nucleotides between 398 to 869 in *Antilope cervicapra* and *Felis catus*; however, 399 to

870 in *Homo sapiens sapiens* species. Except at few positions (marked as star (\*)) in Table

2, the nucleotide sequences of this fragment are highly variable amongst the animal species, revealing the identity of the biological material belonging to that of an unknown animal origin by the procedure invented by us. As for identity of this fragment we are

considering *Antilope cervicapra* as a representative species, and the sequence the above fragment of cytochrome b gene of *Antilope cervicapra* is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*

"taccatgaggacaaatatctttgaggagcaacagtcatccaatcccttcagcaatcccatacatcggtacaaaccttaga  
 5 atgaatctgaggagggttctcagtagataaagcaacccttacccgattttgccttcactttatcctccatttatcattgcagccctt  
 accatagtacacactactgtttctcacgaaacaggatccaacaacccacaggaatctcatcagacgcagacaaaa::ccatcccc  
 ccctactacactatcaaagatatcctaggagctctactattaatttaaccctatgctctagtcctattctcaccggacctgcitggag  
 acccagacaactatacaccagcaaacccacttaatacacccccacatatcaagccgaatgatacttcctattgcatacgaatcct  
 ccgatcaattctaacaacttaggagg

- 10 Table 2 presents the alignment of the above fragment of cytochrome b gene of 221 animal species. Each species in table 2 has been represented by a unique code, which is decoded in Table 1. We selected these species to represent the vast range of animal families of distant orders. Of 221 species, about 65 were the protected/endangered or rare species listed in Wildlife (Protection) Act , 1972 (Central Act NO 53 of 1972). These species are marked  
 15 with symbol (\*) in Table 1. The NCBI accession number refers to its registration number in NCBI database and the number in superscript represent the reference cited. Based on the aligned cytochrome b sequences of different 221 animal species the primers designed were as follow:

Primers name	Sequence (5'-3')
--------------	------------------

- 20 'mcb398' "TACCATGAGGACAAATATCATTCTG"  
 'mcb869' "CCTCCTAGTTGTTAGGGATTGATCG"

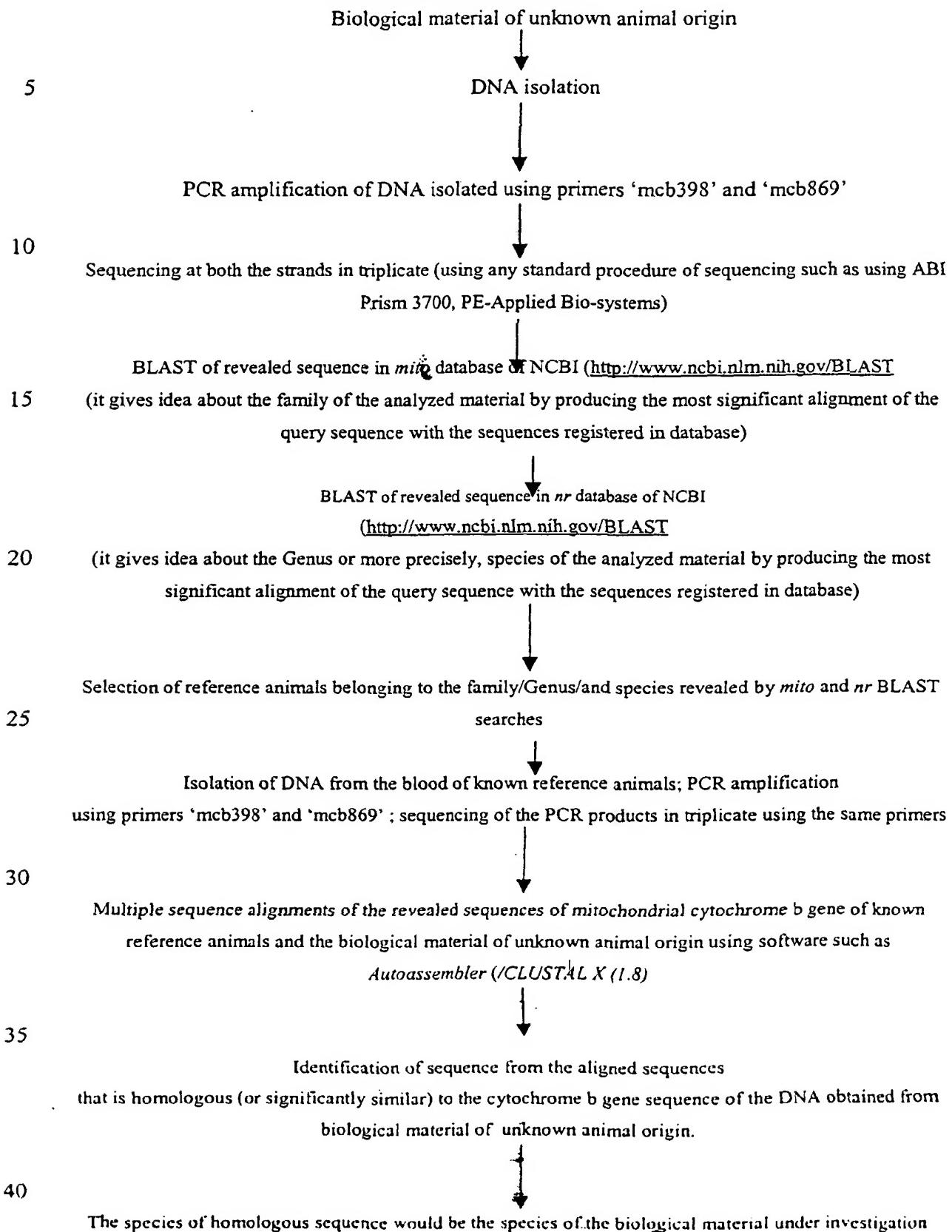
**Tables 2, 10 and 11**, respectively, demonstrates that the 3' ends of the primers are highly conserved amongst all the animal species analyzed *in-silico* (In total 221 animal species listed in Table 1 and about 500 species listed in Tables 10 and 11, respectively) Also, the  
 25 5' end of the primers were selected within the conserved region of cytochrome b gene to improve the probability and stability of match of the primers to their target sequences (i.e. the above mentioned 472 bp fragment of cytochrome b gene). The primers were thoroughly checked for internal stabilities, loop or dimer formation using different software viz., 'Amplify (1.2)', 'Primer3' (<http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi>) as well as manually. . We assigned the P,S score (P=Probability of match, S=Stability of match) to the primers for each template using the software *Amplify* (1.2). The higher scores of P and S ensure a good amplification if all other conditions standard (which are mentioned under 'Example 3') are optimum. The Highest score for 'mcb398' was 98.63 (i.e. the situation where the primer has perfect match with template);

however, the highest P, S for 'mcb869' was recorded as 98, 68 for a complete match between the primer and template. The lowest P,S score observed for 'mcb398' was 81,50 for species *Talpa europaea* whereas 'mcb869' had a high P, S score for this species (92, 57). The another species which have lowest P, S score for one of the two primers were 5 *Eumeces egregios* and *Equus aious*. *Eumeces egregios* had P, S score 86, 55 and 73,51 for 'mcb398' and 'mcb869', respectively; however, the P, S score of *Equus aious* was calculated as 91,61 and 73, 51 for 'mcb398' and 'mcb869', respectively. All other animals had higher P, S scores then the above mentioned species. To ensure that these primers would work efficiently with the DNA template from the animals having the lowest P, S 10 score for one of the primers, we designed an another experiment to validate the lower limits of one of the two primers sufficient for efficient amplification in PCR. We designed an another primer pair (AFF= 5'tagttagaatgaatctgaggagg3' and AFR=5'atgcaaataggaagtatcattc3'.) having more mis-pairing at their annealing sites (but not at ends), therefore have less internal stability and lower P, S scores for its templates (listed 15 in Table 9). The P,S scores of 'AFF' and 'AFR' were as calculated as low as 41 and 49 for *Platanista gangetica* and *Sus scrofa* These species were amplified efficiently using the primers 'AFF' and 'AFR' (results shown in Figure 3) (keeping all other conditions standard i.e. the conditions mentioned in 'Example 3'). The lowest P,S scores (86, 55 and 73,51 for species *Eumeces egregios*) for our primers 'mcb398' and 'mcb869', 20 respectively, were higher then the above range of combined P, S scores of 'AFF' and 'AFR' for species *Sus scrofa* (87, 52 and 87, 41), which was efficiently amplified by the primers 'AFF' and 'AFR'. It gives an indication that the primers 'mcb 398' and 'mcb 869' would work with all the species including *Eumeces egregios* efficiently to give rise to the expected product in PCR. This experiment confirmed that the primers 'mcb398' and 'mcb 25 869' are capable of amplifying the cytochrome b fragment of most of the animal species in a universal manner.

For further confirmation of universal nature of our primers, we blasted the sequence of our primers against the *mito* and *nr* databases of NCBI using BLAST software. The results of these analyses are shown in Tables 10, and 11, respectively.

30 Finally, the universal nature of the primers was tested in our laboratory with some more animal species listed in Table 12. These primers amplified all the animal species efficiently, giving rise to the band of expected size (472 bp). The results are shown in Figure 4. This experiments substantiated the results of P,S analysis and other *in-silico* analyses to show that the primers 'mcb398' and 'mcb 869' are universal primers.

The flow chart of establishing identity of the species of biological material of unknown animal origin using primers 'mcb398' and 'mcb869'



## Examples

### Example 1

Example for identification of a fragment of cytochrome b gene fulfilling the requirements of columns 1, 2 and 3 mentioned under sub-heading 'Objectives of invention' of heading

5 'Brief summary of invention'

The cytochrome b molecule has very vastly been used in molecular taxonomic studies.

Being a slow evolving gene, It has a tremendous information in its nucleotide sequences to distinguish the animals to their family, genus and species sources<sup>1-65</sup>. A vast database of the sequences of cytochrome b gene of different animal species has accumulated in the *nr*

10 and *mito* databases of NCBI. We have explored these qualities of cytochrome b gene to establish the identity of confiscated remains of unknown animal origin to its family, genus and species sources. For this purpose, we have identified a fragment of cytochrome b gene which is highly polymorphic inter-specifically, however, it is monomorphic among the individual of same species, therefore it can group the individual of an unknown species

15 with the known individuals of reference species to which it belongs. In order to amplify this fragment from DNA isolated form any unknown origin, it was necessary that it remain flanked with the highly conserved sequences amongst a vast range of animal families. To identify such a unique fragment within the cytochrome b gene, we aligned the sequences of 221 distantly related animal species (listed in Table 1) representing various families using

20 software CLUSTAL X (1.8). These sequences were obtained from public database iNCBI (<http://www.ncbi.nlm.nih.gov>). The aligned data was examined carefully for the conserved sites amongst all the species included in *in-silico* analysis. We identified a fragment (472 bp) of cytochrome b gene that was fulfilling all the requirements mentioned above and also under column 1, 2 and 3 of sub-heading 'Objectives of invention'.

25 As for the identity of this fragment we would like to mention that it includes the nucleotides between 398 to 869 in *Antilope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions marked as star (\*) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, giving rise to their unique molecular signature. These molecular signatures are

30 characteristic of its species and form the basis of revealing the identity of the biological material of an unknown animal origin by the procedure invented by us. Considering *Antilope cervicapra* as a representative species, the sequence of this fragment is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*

“taccatgaggacaaatatctttgaggagaacagtcatcaccaatcccttcagcaatcccatacatcggtacaaaccttaga  
atgaatctgaggagggtctcagtagataaagcaacccttacccgatttcgccttccactttatcctccatttatcattgcagccctt  
accatagtacacactactgttctccacgaaacaggatccaacaacccacaggaatctcatcagacgcagacaaaattccattccac  
ccctactacactatcaaagatatcttaggagctactattaatttaaccctcatgctctagtcattctcaccggacctgcitggag  
5 acccagacaactatacaccagcaaacccacttaatacacccacatatacagccgaatgataacttcctattgcatacgcaatcct  
ccgatcaattcctaacaaacttaggagg”

**Example 2:**

Example for development of universal primers to amplify the fragment identified mentioned under ‘Example 1’.

10

A pair of universal primer was designed which has the following features:

1. It targets the fragment identified (mentioned under ‘Example 1’) to amplify it in polymerase chain reaction (PCR).
2. Its 3’ and 5’ ends that are highly conserved (marked as star (\*) in Table 2), amongst a vast range of animal species ensuring the amplification of the fragment mentioned above in a universal manner. The sequencing of the fragment amplified by these primes reveals the molecular signature of the species of analyzed material, which on comparison with the sequences of the known reference animals reveals the identity of the species of unknown biological material under investigation.
- 15 3. The tm (melting temperature) of both primers was almost similar (about 58 degree centigrade) ensuring the significant annealing of both the primers to its template, therefore significant amplification of targeted region in PCR.
- 20 4. The internal stability and P, S, score of the primers were ensured higher while designing it. The possibilities of internal loop formation, dimmer formation etc were also excluded by selecting its sequence uniquely. This ensured that the primer would be a good primer to be used in PCR for amplification of DNA from unknown animal origin.
- 25 5. The 3’ end of the primers were ensured to have either ‘G’ or ‘C’ to increase the probability of strong bonding at its 3’ends, which is necessary for efficient amplification of DNA template in PCR. It also strengthens the universal nature of the primer.
- 30 6. The sequences of the primers were ensured to be unique so that it does not give rise to non-specific and spurious products in PCR leading to confusion. It improved the efficiency and quality of the technique invented by us.

7. These primers were named as 'mcb398' and 'mcb869' because of its property to amplify a region of mitochondrial cytochrome b gene between nucleotides 398 to 869 of *Antilope cervicapra*, a representative animal species for this invention. We took this animal species as representative species because the idea of developing such a novel primers came in the mind of inventors while they were working on the genome of this animal in Centre for Cellular and Molecular Biology, Hyderabad, India.

5           8. The sequences of the universal primers invented are as follows:

Primers name	Sequence (5'-3')
'mcb398'	"TACCATGAGGACAAATATCATTCTG"
'mcb869'	"CCTCCTAGTTGTTAGGGATTGATCG"

10           **Example 3:**

Example for development of universal PCR conditions to ensure the amplification of a template of any unknown origin in PCR, hence strengthening the universal nature of the 15 technique invented by us

The PCR conditions developed had the following unique features:

1 These were capable of amplifying the DNA template of any animal origin in an universal manner using the universal primers mentioned under 'Example 2'.

20           2. The conditions were selected to ensure the comparable annealing temperature for both the primers i.e. 'mcb398' and 'mcb869'.

25           3. The PCR conditions standardized herewith are universal; therefore, the possibility of PCR failure with a template of unknown origin due to non-standard conditions is excluded. It ensures the universal nature of our technique to be used in wildlife forensics.

4. The universal conditions mentioned above are:

Amplification reactions should be carried out in 20  $\mu$ l reaction volume containing approximately 20 ng of template DNA, 100 $\mu$ M each of dNTPs, 1.25 pmole of each primer, 30 1.5mM MgCl<sub>2</sub>, 0.5 unit of AmpliTaq Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed should be: an initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35<sup>th</sup> cycles should be held for 10 min.

**Example 4:**

Establishing the universal nature of our primer and experimental evidences to demonstrate the universal nature of primers:

The universal nature of the primers 'mcb398' and 'mcb 869' was ensured by the following

5 measures:

(a) Selecting the primers from the aligned cytochrome b gene sequences of 221 animal of distantly related species:

The cytochrome b gene sequences (1140 bp) were aligned using software *CLUSTAL X* (1.8). The region of cytochrome b gene that was most conserved amongst 221 animal  
10 species was selected to design the primers.

(b) Selecting the 3' and 5' ends of the primers at the highly conserved positions of cytochrome b gene:

The 3' and 5' ends of the primers were ensured to anneal to a highly conserved position amongst 221 animal species representing a vast range of animal families. It was done to ensure an efficient amplification of all the species in PCR. These positions are shown with star (\*) mark in Table 2.  
15

(c) Ensuring either 'G' or 'C' at the 3' end of the primers:

It was ensured the primers to have either 'G' or 'C' at its 3' ends as these are the nucleotides that ensure the strong bonding at the 3' ends of the primers due to three  
20 hydrogen bonds while pairing with each other. The strong bonding at 3' ends helps the primers to anneal properly with its template resulting in significant amplification in PCR.

(d) Selecting the sequences of the primers to ensure a higher internal stability, higher P, S score, and no primer dimmer and loop formation:

The sequences of the primers were selected to have a high P, S score for a vast range of animal species (Shown in Table 1). The care was taken to exclude the possibilities of loop  
25 or primer dimmer formation that could reduce the efficiency of the primers in PCR.

(e) Selecting the sequence of the primers with a comparable melting temperature:

The sequences of the primers were selected to have a comparable melting temperature so that these could work together to amplify a DNA template in PCR at a similar annealing  
30 temperature. The melting temperature of both the primers was about 58 degree centigrade and the annealing temperature used in PCR is 51 degree centigrade.

Experimental evidences to demonstrate the universal nature of primers:

(1) Evidence from *In-silico* analysis :

(a) Selecting the primers within the most conserved region of mitochondrial cytochrome b gene

As mentioned above, the primers were designed to anneal within a highly conserved region of mitochondrial cytochrome b gene fragment of 472 bp. Table 2 presents the alignment of the above fragment of cytochrome b gene of 221 animal species representing a vast range of animal families. The conserved positions of nucleotide sequences are shown with star (\*) mark in Table 2

Table 2 also demonstrates that the 3' ends of the primers are highly conserved amongst all the animal species analyzed *in-silico*. In the aligned sequences, the conserved nucleotides are marked with symbol (\*). Also, the 5' end of the primers were selected within the conserved region of cytochrome b gene to improve the probability and stability of match of the primers to their target sequences (i.e. the above mentioned 472 bp fragment of cytochrome b gene). The primers were thoroughly checked for internal stabilities, loop or dimer formation using different software viz., 'Amplify (1.2)', 'Primer3' (<http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi>) as well as manually.

(b) P, S, score analysis:

and lower P, S scores for its templates (listed in Table 9). The P,S scores of 'AFF' and 'AFR' were as calculated as low as 41 and 49 for *Platanista gangetica* and *Sus scrofa*. These species were amplified efficiently using the primers 'AFF' and 'AFR' (results shown in Figure 3) (keeping all other conditions standard i.e. the conditions mentioned in  
5 'Example 3'). The lowest P,S scores (86, 55 and 73,51 for species *Eumeces egredios*) for our primers 'mcb398' and 'mcb869', respectively, were higher then the above range of combined P, S scores of 'AFF' and 'AFR' for species *Sus scrofa* (87, 52 and 87, 41), which was efficiently amplified by the primers 'AFF' and 'AFR'. It gives an indication  
10 that the primers 'mcb 398' and 'mcb 869' would work with all the species including *Eumeces egredios* efficiently to give rise to the expected product in PCR. This experiment confirmed that the primers 'mcb398' and 'mcb 869' are capable of amplifying the cytochrome b fragment of most of the animal species in a universal manner.

© BLAST analysis:

15 The sequences of primers 'mcb398' and 'mcb869' were blasted against mito and nr databases of NCBI to see its significant alignments with the sequences registered in GenBank. As expected, the most significant alignments of the sequences were found with the cytochrome b gene regions (within the 472 bp fragment mentioned in 'Example 1') of different animal species. This analysis also showed that the 3' as well as 5' ends of the  
20 primers were highly conserved amongst a vast range of animal species, confirming the universal nature of the primers (Tables 10 and 11, respectively)

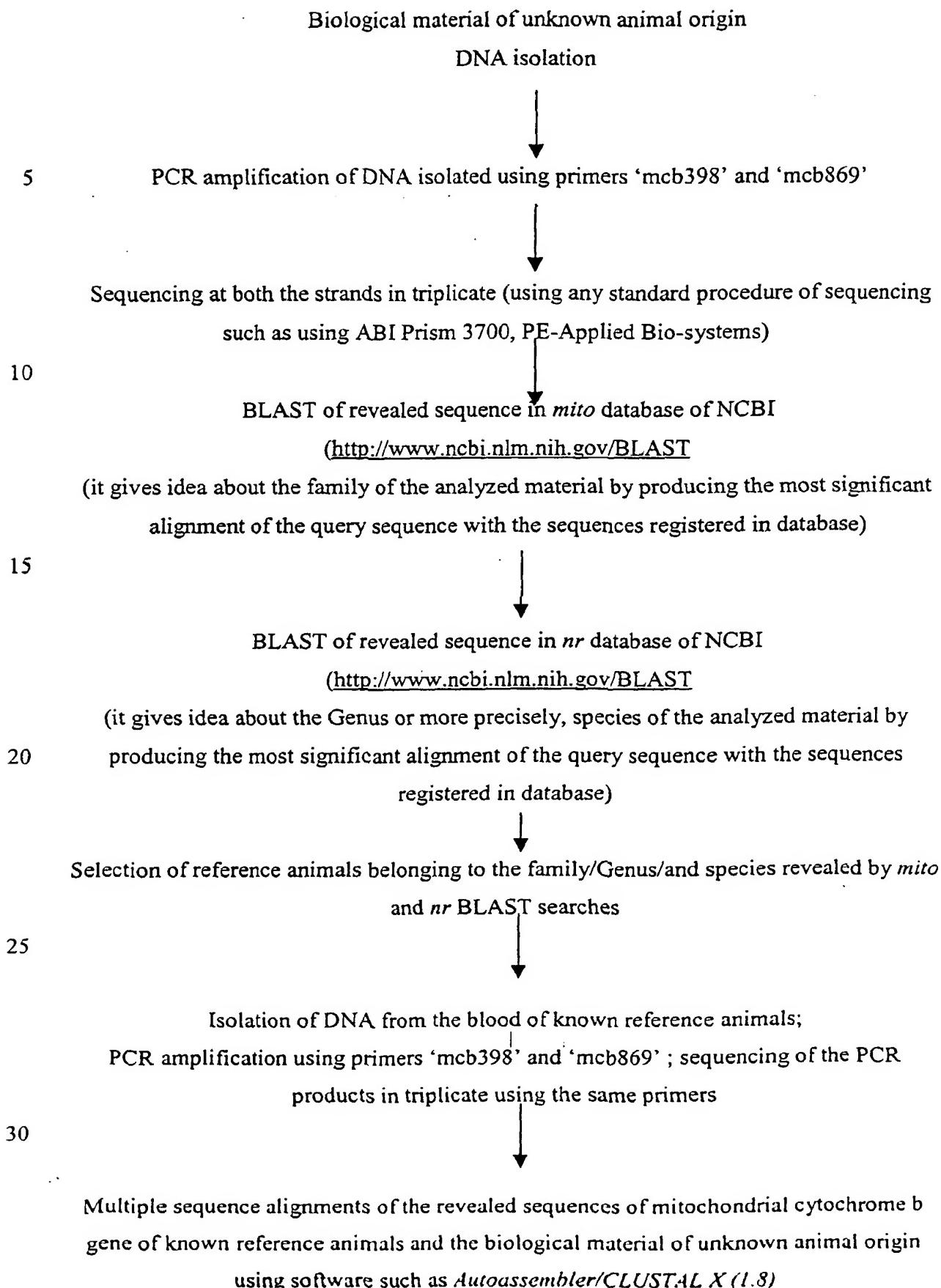
(2) Evidence from bench work/experiments done in laboratory conditions:

The DNA from different animals belonging to distantly related species (mentioned in  
25 Table 12) was isolated and subjected to PCR amplification using the primers invented by us i.e. the primers 'mcb398' and 'mcb869'. The PCR products amplified were resolved in agarose gel by electrophoresis and visualized under UV light. The PCR products of expected size (472bp) were obtained from all the animals confirming the universal nature of our primers. These results are shown in Figure 4.  
30

**Example 5:**

Example to establish the identity of confiscated remains from unknown animal origin using the universal primers 'mcb398' and 'mcb869'.

The step-wise procedure to establish the identity of the biological material from an  
35 unknown animal source is mentioned below:



↓

Identification of sequence from the aligned sequences  
that is homologous (or significantly similar) to the cytochrome b gene sequence of the  
DNA obtained from biological material of  
unknown animal origin.

↓

The species of homologous sequence would be the species of the biological material under  
investigation

↓

Application of the above information for the objectives mentioned in columns 7-13 under  
sub-heading 'Objective of invention' of heading 'Summary of invention'

15   **Example 6:**

The actual execution of the technique invented

As a first application and to demonstrate the ease and utility of this method, we investigated a case of forensic identification submitted at our laboratory to seek scientific opinion on animal hunting evidence. In this case, we received the half burned remains of  
20 an unknown animal, confiscated by the crime investigation agencies. The DNA was isolated from the above material following standard methods<sup>74</sup> and subjected to PCR amplification using the primers mentioned above (viz., 'mcb398' and 'mcb869'). Amplification reactions were carried out in 20 µl reaction volume containing 20 ng of template DNA, 100µm each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl<sub>2</sub>, 0.5 unit  
25 of AmpliTaq Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed were: an initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35<sup>th</sup> cycles was held for 10 min.

30 The PCR products obtained were sequenced in automated work station (ABI Prism 3700, PE-Biosystems) on both strands in triplicate and the sequence resolved (328 bp, shown in Figure 1a) was blasted against *mito* databases of NCBI using BLAST program<sup>73</sup>. The most significant alignment (bits Value 365, E value e<sup>-101</sup>) of this sequence was produced with the cytochrome b gene sequence of *Felis catus*. (Table 3) indicating that species of

analyzed material belongs to family felidae. Further, the above sequence revealed from the confiscated remain was blasted against *nr* databases of NCBI using BLAST program. The most significant alignment (bits Value 603, E value  $e^{-170}$ ) of this sequence was produced with the cytochrome b gene sequence of *Panthera pardus* (Table 4), indicating the identity 5 of the analyzed material as that of a *Panthera pardus* source. Based on this information, we selected the reference animals listed in Table 5 representing different species and subspecies of felidae. The DNA isolated from reference animals was amplified and sequenced on both strands in triplicate using the primer pair mentioned above. Consensus 10 sequences obtained were aligned using program *CLUSTAL X (1.8)* (Table 6). Sequence comparisons identified 113 variable sites in total amongst all animals analyzed (Table 7). Pair-vise comparisons of sequences were performed to find out the variation among different animals investigated. All the species investigated were differentiated by their unique nucleotides sequences. The molecular signatures of different reference animals were compared with the molecular signature of the confiscated skin 'adil.flesh'. Table 7 15 demonstrate that the maximum similarity of the adil.flesh with 'gz11' i.e. known Leopard (*Panthera pardus*) species, indicating the identity of the adil.flesh, the confiscated skin, as that of a *Panthera pardus* origin. We also calculated the similarity matrix showing the pair-vise similarity amongst the animal species under investigation using *PHYLIP* software. This matrix is shown in Table 8. It demonstrates that the animals belonging to different 20 species had more variation; however, the animals of same species had maximum similarity among their cytochrome b sequences. The cytochrome b gene sequence of DNA isolated from confiscated material had maximum similarity with the sequences obtained from known Leopard source(99.7%, and 98.2 with 'gz11' and 'gz21', respectively); establishing the identity of the source of confiscated material as that of a Normal leopard (*Penthera pardus*) species. The step-vise procedure involved in above analysis is illustrated in Figure 25 1a, 1b and 1c, respectively.

Thus, the primers invented by us can generate the molecular signature from any biological material of unknown animal origin, which actually is the characteristic of its family, genus and more precisely, the species. When these signatures are compared *in-silico* with the 30 signatures already available in public databases (viz., GenBank, NCBI database etc) using *BLAST* software<sup>73</sup>, it indicates identity of the family, genus or species of the analyzed material, which in turn is confirmed practically by comparing with the reference animals of the revealed family, genus or species, by including them in the further analysis by the primers 'mcb398' and 'mcb869'. Application of the information revealed could be in

fulfilling the requirements of objectives mentioned in columns 7-13 under sub-heading 'Objective of invention' of heading 'Summary of invention'

The method of the invention can be used to establish the identity of confiscated animal parts and products is one of the key requirements of wildlife identification in forensics. It

5 is needed to establish the crime with the criminal beyond a reasonable doubt to avoid the human violation of wildlife resources. Various morphological biochemical and molecular approaches have been given for this purpose; however, none of the current methods is universally applicable to detect the mutilated animal remains of unknown origin. We have

identified a fragment on the mitochondrial cytochrome b gene, which has enormous information to differentiate among various animal species back to the family, genus and species sources. We have also found that this fragment is flanked by the highly conserved sequences amongst a vast range of animal species. We invented a pair of universal primer

10 that can amplify this fragment of DNA isolated from the biological material of an unknown animal origin in polymerase chain reaction (PCR) to reveal its identity at species and sub-species sources. This novel invention has great potential to revolutionize the whole scenario of wildlife forensic identification and crime investigation.

15

Table 1. The animal species included in the study for *in-silico* analysis

SN.	Code	Name	NCBI accession #	*P,S/F	*P,S/R
1	aep.mel	<i>Aepyceros melampus</i>	AF036289 <sup>1</sup>	97, 60	94, 62
2	ore.ore	<i>Oreotragus oreotragus</i>	AF036288 <sup>1</sup>	88, 52	94, 62
3	add.nas	<i>Addax nasomaculatus</i>	AF034722 <sup>2</sup>	97, 60	95, 66
4	ory.dam	<i>Oryx damah</i>	AJ222685 <sup>1</sup>	90, 58	95, 66
5	hip.equ	<i>Hippotragus equinus</i>	AF022060 <sup>3</sup>	98, 63	85, 55
6	alc.bus	<i>Alcelaphus buselaphus</i>	AJ222681 <sup>1</sup>	97, 60	98, 68
7	sig.lic	<i>Sigmoderos lichtensteinii</i>	AF034967 <sup>4</sup>	97, 60	98, 68
8	bea.hun	<i>Beatragus hunteri</i>	AF034968 <sup>4</sup>	97, 60	94, 62
9	dam.lun	<i>Damaliscus lunatus</i>	AF016635 <sup>3</sup>	97, 60	77, 55
10	con.tau	<i>Connochaetes taurinus</i>	AF016638 <sup>3</sup>	82, 56	93, 62
11	bis.bon	<i>Bison bonasus</i>	Y15005 <sup>5</sup>	90, 58	87, 63
12	bos.gru	<i>Bos grunniens</i> *	AF091631 <sup>6</sup>	90, 58	94, 62
13	bos.tra	<i>Bos tragocamelus</i> *	AJ222679 <sup>1</sup>	90, 58	95, 66
14	buba.bub	<i>Bubalus bubalis</i> *	D34637 <sup>7</sup>	97, 60	93, 64
15	bub.min	<i>Bubalus mindorensis</i>	D82895 <sup>8</sup>	97, 60	87, 62
16	tra.ang	<i>Tragelaphus angasii</i>	AF091633 <sup>6</sup>	97, 60	87, 63
17	tra.eur	<i>Tragelaphus eurycerus</i>	AF036276 <sup>1</sup>	90, 58	97, 64
18	nem.cau	<i>Nemorhaedus caudatus</i> *	U17861 <sup>9</sup>	95, 61	93, 59
19	pse.nay	<i>Pseudois nayaur</i>	AF034732 <sup>2</sup>	89, 55	89, 59
20	amm.lem	<i>Ammotragus lervia</i>	AF034731 <sup>2</sup>	94, 58	97, 63
21	cap.fal	<i>Capra falconeri</i> *	D84202 <sup>10</sup>	98, 63	95, 66
22	cap.ibex	<i>Capra ibex</i> *	AF034735 <sup>2</sup>	98, 63	89, 58
23	hem.jem	<i>Hemitragus jemlahicus</i> *	AF034733 <sup>2</sup>	95, 61	90, 61
24	rup.pyr	<i>Rupicapra pyrenaica</i>	AF034726 <sup>2</sup>	95, 61	89, 59
25	rup.rup	<i>Rupicapra rupicapra</i>	AF034725 <sup>2</sup>	95, 61	94, 64
26	pan.hod	<i>Pantholops hodgsoni</i>	AF034724 <sup>2</sup>	98, 63	95, 66
27	bud.tax.tax	<i>Budorcas taxicolor taxicolor</i> *	U17868 <sup>9</sup>	90, 58	95, 66
28	ovi.amm	<i>Ovis ammon</i> *	AF034727 <sup>2</sup>	98, 63	97, 64
29	ovi.vig	<i>Ovis vignei</i> *	AF034729 <sup>2</sup>	98, 63	97, 64
30	cap.cri	<i>Capcornis crispus</i> *	AJ304502 <sup>11</sup>	98, 63	94, 63
31	ovi.mos	<i>Ovibos moschatus</i>	U17862 <sup>9</sup>	98, 63	92, 61
32	ore.ame	<i>Oreamnos americanus</i>	AF190632 <sup>12</sup>	98, 63	94, 62
33	cep.dor	<i>Cephalophus dorsalis</i>	AF091634 <sup>6</sup>	97, 58	90, 61
34	cep.max	<i>Cephalophus maxwellii</i>	AF096629 <sup>13</sup>	97, 60	88, 53
35	alc.alc	<i>Alces alces</i>	AJ000026 <sup>14</sup>	95, 61	93, 59
36	hyd.ine	<i>Hydropotes inermis</i>	AJ000028 <sup>14</sup>	97, 60	90, 63
37	mun.mun	<i>Muntiacus muntjak</i> *	AF042713 <sup>15</sup>	90, 58	93, 64
38	cer.ele.kan	<i>Cervus elaphus kansuensis</i> *	AB021098 <sup>16</sup>	98, 63	82, 59
39	cer.ele.xan	<i>Cervus elaphus xanthopygus</i> *	AB021097 <sup>16</sup>	98, 63	82, 59
40	cer.ele.can	<i>Cervus elaphus canadensis</i> *	AB021096 <sup>16</sup>	98, 63	90, 61
41	cer.nip.cc	<i>Cervus nippon centralis</i>	AB021094 <sup>17</sup>	98, 63	90, 61
42	cer.nip.ye	<i>Cervus nippon yesoensis</i>	AB021095 <sup>17</sup>	98, 63	90, 61
43	cer.nip.ke	<i>Cervus nippon keramiae</i>	AB021091 <sup>17</sup>	98, 63	90, 61

44 cer.nip.pu	<i>Cervus nippon pulchellus</i>	AB021090 <sup>16</sup>	98, 63	90, 61
45 cer.nip.ni	<i>Cervus nippon nippon</i>	AB021093 <sup>16</sup>	98, 63	90, 61
46 cer.elas.c	<i>Cervus elaphus scoticus</i>	AB021099 <sup>16</sup>	98, 63	90, 61
47 cer.dam	<i>Cervus dama</i>	AJ000022 <sup>14</sup>	98, 63	88, 53
48 ran.tar	<i>Rangifer tarandus</i>	AJ000029 <sup>14</sup>	98, 63	89, 57
49 mos.fus	<i>Moschus fuscus*</i>	AF026888 <sup>17</sup>	90, 59	90, 61
50 mos.leu	<i>Moschus leucogaster*</i>	AF026889 <sup>17</sup>	90, 59	90, 61
51 mos.chr	<i>Moschus chrysagaster*</i>	AF026887 <sup>17</sup>	90, 59	90, 61
52 mos.ber	<i>Moschus berezovskii*</i>	AF026886 <sup>17</sup>	90, 59	90, 61
53 mos.mos	<i>Moschus moschiferus*</i>	AF026883 <sup>17</sup>	90, 59	92, 61
54 kob.ell	<i>Kobus ellipsiprymnus</i>	AF022059 <sup>3</sup>	91, 61	95, 66
55 kob.meg	<i>Kobus megaceros</i>	AJ222686 <sup>1</sup>	91, 61	83, 56
56 red.aru	<i>Redunca arundinum</i>	AF096628 <sup>13</sup>	91, 61	94, 62
57 red.ful	<i>Redunca fulvorufa</i>	AF036284 <sup>1</sup>	89, 57	94, 62
58 neo.mos	<i>Neotragus moschatus</i>	AJ222683 <sup>1</sup>	89, 57	94, 62
59 pel.cap	<i>Pelea capreolus</i>	AF022055 <sup>3</sup>	91, 61	90, 61
60 ant.cer	<i>Antilope cervicapra*</i>	AF022058 <sup>3</sup>	82, 56	93, 64
61 sai.tat	<i>Saiga tatarica</i>	AF064487 <sup>18</sup>	91, 61	92, 61
62 gaz.dam	<i>Gazella dama</i>	AF025954 <sup>3</sup>	91, 61	92, 61
63 our.our	<i>Ourebia ourebi</i>	AF036288 <sup>1</sup>	82, 56	82, 59
64 gaz.gaz	<i>Gazela gazella*</i>	AJ222682 <sup>1</sup>	91, 61	89, 57
65 rap.mel	<i>Raphicerus melanotis</i>	AF022053 <sup>3</sup>	81, 54	80, 50
66 mad.kir	<i>Madoqua kirkii</i>	AF022070 <sup>3</sup>	90, 58	97, 65
67 ant.ame	<i>Antilocapra americana</i>	AF091629 <sup>6</sup>	98, 63	98, 68
68 tra.jav	<i>Tragulus javanicus*</i>	D32189 <sup>19</sup>	86, 57	86, 59
69 tra.nap	<i>Tragulus napu*</i>	X56288 <sup>20</sup>	81, 52	93, 58
70 bal.acu	<i>Balaenoptera acutorostrata</i>	X75753 <sup>21</sup>	89, 56	97, 61
71 bal.bon	<i>Balaenoptera bonaerensis</i>	X75581 <sup>21</sup>	89, 56	93, 59
72 bal.bor	<i>Balaenoptera borealis*</i>	X75582 <sup>21</sup>	89, 56	93, 59
73 bal.edi	<i>Balaenoptera edeni</i>	X75583 <sup>21</sup>	89, 56	88, 54
74 esc.rob	<i>Eschrichtius robustus*</i>	X75585 <sup>21</sup>	97, 61	86, 57
75 bal.mus	<i>Balaenoptera musculus*</i>	NC_001601 <sup>22</sup>	97, 57	93, 59
76 meg.nov	<i>Megaptera novaeangliae*</i>	X75584 <sup>21</sup>	97, 61	94, 63
77 bal.phy	<i>Balaenoptera physalus*</i>	NC_001321 <sup>22</sup>	97, 57	94, 63
78 cap.mar	<i>Caperea marginata</i>	X75586 <sup>21</sup>	93, 55	91, 53
79 cep.com	<i>Cephalorhynchus commersonii</i>	AF084073 <sup>24</sup>	85, 51	88, 55
80 cep.eut	<i>Cephalorhynchus eutyropis*</i>	AF084072 <sup>24</sup>	85, 51	92, 59
81 lag.obl	<i>Lagenorhynchus obliquidens</i>	AF084067 <sup>24</sup>	94, 59	92, 59
82 cep.heu	<i>Cephalorhynchus heavisidii</i>	AF084070 <sup>24</sup>	89, 56	97, 63
83 cep.hec	<i>Cephalorhynchus hectori*</i>	AF084071 <sup>24</sup>	89, 56	92, 59
84 lag.aus	<i>Lagenorhynchus australis</i>	AF084069 <sup>24</sup>	86, 54	92, 59
85 lag.cru	<i>Lagenorhynchus cruciger</i>	AF084068 <sup>24</sup>	86, 54	92, 59
86 lag.obs	<i>Lagenorhynchus obscurus</i>	AF084066 <sup>24</sup>	86, 54	92, 59
87 lis.bor	<i>Lissodelphis borealis</i>	AF084064 <sup>24</sup>	85, 51	92, 59
88 lis.per	<i>Lissodelphis peronii</i>	AF084065 <sup>24</sup>	86, 54	92, 59
89 glo.mac	<i>Globicephala macrorhynchus</i>	AF084055 <sup>24</sup>	94, 59	88, 55
90 glo.mel	<i>Globicephala melas</i>	AF084056 <sup>24</sup>	94, 59	88, 55
91 fer.att	<i>Feresa attenuata*</i>	AF084052 <sup>24</sup>	94, 59	92, 59

92 pep.ele	<i>Pepinocephala electra</i> *	AF084053 <sup>24</sup>	94, 59	88, 55
93 gra.gri	<i>Grampus griseus</i>	AF084059 <sup>24</sup>	97, 61	89, 59
94 pse.cra	<i>Pseudorca crassidens</i> *	AF084057 <sup>24</sup>	94, 59	92, 59
95 lag.acu	<i>Lagenorhynchus acutus</i>	AF084075 <sup>24</sup>	98, 63	89, 59
96 orci.bre	<i>Orcinus orca</i>	AF084061 <sup>24</sup>	86, 57	82, 52
97 orca.bre	<i>Orcaella brevirostris</i>	AF084063 <sup>24</sup>	86, 57	91, 54
98 del.cap	<i>Delphinus capensis</i>	AF084087 <sup>24</sup>	96, 54	97, 63
99 del.tro	<i>Delphinus tropicalis</i>	AF084088 <sup>24</sup>	97, 57	97, 63
100 del.del	<i>Delphinus delphis</i>	AF084085 <sup>24</sup>	97, 57	97, 63
101 sten.cly	<i>Stenella clymene</i>	AF084083 <sup>24</sup>	97, 57	97, 63
102 sten.coe	<i>Stenella coeruleoalba</i>	AF084082 <sup>24</sup>	97, 57	97, 66
103 tur.adu	<i>Tursiops aduncus</i>	AF084092 <sup>24</sup>	97, 57	97, 63
104 sten.fro	<i>Stenella frontalis</i>	AF084090 <sup>24</sup>	97, 57	97, 63
105 saus.chi	<i>Sousa chinensis</i>	AF084080 <sup>24</sup>	97, 57	88, 59
106 sten.lon	<i>Stenella longirostris</i>	AF084103 <sup>24</sup>	97, 61	97, 63
107 turs.tru	<i>Tursiops truncatus</i>	AF084095 <sup>24</sup>	97, 57	96, 59
108 lage.alb	<i>Lagenorhynchus alborostris</i>	AF084074 <sup>24</sup>	97, 61	97, 66
109 sten.bre	<i>Steno bredanensis</i>	AF084077 <sup>24</sup>	97, 61	94, 64
110 sota.flu	<i>Sotalia fluviatilis</i>	AF304067 <sup>25</sup>	97, 61	97, 63
111 del.leu	<i>Delphinapterus leucas</i>	U72037 <sup>26</sup>	97, 61	95, 66
112 mono.mon	<i>Monodon monoceros</i>	U72038 <sup>26</sup>	97, 61	95, 66
113 plat.gan	<i>Platanista gangetica</i> *	AF304070 <sup>25</sup>	97, 61	86, 59
114 plat.min	<i>Platanista minor</i> *	X92543 <sup>27</sup>	97, 61	86, 59
115 kogi.bre	<i>Kogia breviceps</i>	U72040 <sup>26</sup>	97, 59	90, 63
116 kogi.sim	<i>Kogia simus</i>	AF304072 <sup>25</sup>	96, 55	92, 63
117 phys.cat	<i>Physeter catodon</i>	AF304073 <sup>25</sup>	97, 57	80, 58
118 lipo.vex	<i>Lipotes vexillifer</i> *	AF304071 <sup>25</sup>	89, 56	88, 53
119 phoc.sin	<i>phocoena sinus</i>	AF084051 <sup>24</sup>	87, 49	92, 62
120 bera.bai	<i>Berardius bairdii</i>	X92541 <sup>27</sup>	96, 55	90, 59
121 ziph.cat	<i>Ziphius cavirostris</i>	X92540 <sup>27</sup>	97, 61	89, 57
122 meso.eur	<i>Mesoplodon europaeus</i>	X92537 <sup>27</sup>	97, 57	90, 61
123 meso.bid	<i>Mesoplodon bidens</i>	X92538 <sup>27</sup>	97, 61	92, 61
124 meso.den	<i>Mesoplodon densirostris</i>	X92536 <sup>27</sup>	91, 61	94, 63
125 hype.amp	<i>Hyperoodon ampullatus</i> *	X92539 <sup>27</sup>	97, 61	90, 65
126 meso.per	<i>Mesoplodon peruvianus</i>	AF304074 <sup>25</sup>	97, 61	86, 58
127 pont.blai	<i>Pontoporia blainvilliei</i>	AF304069 <sup>25</sup>	92, 59	88, 55
128 hipp.amp	<i>Hippopotamus amphibius</i>	Y08813 <sup>29</sup>	92, 58	95, 66
129 hex.lib	<i>Hexaprotodon liberiensis</i>	Y08814 <sup>29</sup>	98, 63	97, 66
130 rhin.son	<i>Rhinoceros sondaicus</i> *	AJ245725 <sup>10</sup>	90, 59	87, 61
131 cera	<i>Ceratotherium simum</i>	NC_001808 <sup>11</sup>	90, 59	90, 63
132 dic.sum	<i>Dicerorhinus sumatrensis</i>	AJ245723 <sup>10</sup>	90, 59	86, 57
133 equu	<i>Equus asinus</i>	NC_001788 <sup>11</sup>	91, 61	73, 51
134 baby.bab	<i>Babyrousa babyrussa</i>	ZS0106 <sup>11</sup>	89, 56	85, 56
135 phac.afr	<i>Phacochoerus africanus</i>	ZS0090 <sup>11</sup>	90, 59	87, 54
136 sus.scr.ew	<i>Sus scrofa</i> haplotype EWBJ*	AF136549 <sup>14</sup>	97, 57	83, 54
137 sus.bar	<i>Sus barbatus</i>	ZS0107 <sup>11</sup>	97, 57	85, 55
138 lama.gla	<i>Lama glama</i>	U06429 <sup>11</sup>	89, 55	85, 53
139 lama.gua	<i>Lama guanicoe</i>	Y05512 <sup>11</sup>	88, 54	86, 57

140	vic.vic	<i>Vicugna vicugna</i>	U06430 <sup>35</sup>	89, 55	85, 53
141	cam.bac	<i>Camelus bactrianus</i>	U06427 <sup>35</sup>	94, 58	86, 58
142	arc.for	<i>Arctocephalus forsteri</i>	X82293 <sup>36</sup>	97, 60	87, 64
143	arc.gaz	<i>Arctocephalus gazella</i>	X82292 <sup>36</sup>	94, 58	87, 64
144	eum.jub	<i>Eumetopias jubatus</i>	X82311 <sup>36</sup>	97, 57	86, 57
145	zal.cal	<i>Zalophus californianus</i>	X82310 <sup>36</sup>	89, 55	86, 57
146	odo.ros	<i>Odobenus rosmarus</i>	X82299 <sup>36</sup>	91, 61	81, 52
147	pho.vit	<i>Phoca vitulina</i>	X82306 <sup>36</sup>	90, 58	87, 64
148	pho.fascia	<i>Phoca fasciata</i>	X82302 <sup>36</sup>	98, 63	95, 66
149	pho.gro	<i>Phoca groenlandica</i>	X82303 <sup>36</sup>	92, 59	90, 61
150	cys.cri	<i>Cystophora cristata</i>	X82294 <sup>36</sup>	89, 56	87, 64
151	hyd.lep	<i>Hydrurga leptonyx</i>	X82297 <sup>36</sup>	89, 55	82, 54
152	lep.wed	<i>Leptonychotes weddelli</i>	X72005 <sup>37</sup>	98, 63	91, 66
153	mir.leo	<i>Mirounga leonina</i>	X82298 <sup>36</sup>	89, 55	82, 59
154	eri.bar	<i>Erignathus barbatus</i>	X82295 <sup>36</sup>	89, 56	87, 63
155	mons.ch	<i>Monachus schauinslandi</i>	X72209 <sup>37</sup>	91, 61	87, 60
156	hela.mal	<i>Helarctos malayanus</i> *	U18899 <sup>38</sup>	84, 54	90, 63
157	sel.thi	<i>Selenarctos thibetanus</i> *	AB020910 <sup>39</sup>	89, 57	87, 64
158	ail.ful	<i>Ailurus fulgens</i> *	X94919 <sup>40</sup>	93, 55	87, 64
159	fel	<i>Felis catus</i>	NC_001700 <sup>41</sup>	85, 56	90, 63
160	can	<i>Canis familiaris</i>	NC_002008 <sup>42</sup>	98, 58	84, 54
161	tal	<i>Talpa europaea</i>	NC_002391 <sup>43</sup>	81, 50	92, 57
162	gla.sab	<i>Glaucomys sabrinus</i>	AF011738 <sup>44</sup>	90, 59	82, 54
163	gla.vol	<i>Glaucomys volans</i>	AB030261 <sup>45</sup>	90, 59	87, 60
164	hyl.pha	<i>Hylopetes phayrei</i> *	AB030259 <sup>45</sup>	91, 61	81, 50
165	pet.set	<i>Petinomys setosus</i> *	AB030260 <sup>45</sup>	91, 61	81, 50
166	bel.pea	<i>Belomys pearsonii</i> *	AB030262 <sup>45</sup>	91, 61	87, 64
167	pte.mom	<i>Pteromys momonga</i> *	AB030263 <sup>45</sup>	97, 61	90, 63
168	gala.demi	<i>Galagoides demidoff</i>	AF271411 <sup>46</sup>	97, 58	87, 64
169	pero.pot	<i>Perodicticus potto</i>	AF271413 <sup>46</sup>	97, 60	87, 63
170	gala.mat	<i>Galago matschiei</i>	AF271409 <sup>46</sup>	97, 60	90, 61
171	gala.moh	<i>Galago moholi</i>	AF271410 <sup>46</sup>	97, 57	95, 66
172	oto.gar	<i>Otolemur garnettii</i>	AF271412 <sup>46</sup>	92, 58	87, 60
173	lor.tar	<i>Loris tardigradus</i> *	US3581 <sup>47</sup>	97, 60	93, 59
174	nyc.cou	<i>Nycticebus coucang</i> *	US3580 <sup>47</sup>	97, 60	95, 66
175	mus	<i>Mus musculus</i>	NC_001569 <sup>48</sup>	97, 60	86, 59
176	gorr	<i>Gorilla gorilla</i>	NC_001645 <sup>49</sup>	89, 57	80, 58
177	homo	<i>Homo sapiens sapiens</i>	NC_001807 <sup>50</sup>	96, 55	84, 64
178	dug.dug	<i>Dugong dugong</i> *	U07564 <sup>51</sup>	97, 60	89, 59
179	ele.max	<i>Elephas maximus</i> *	AB002412 <sup>52</sup>	97, 60	76, 57
180	afr.con	<i>Afropavo congensis</i>	AF013760 <sup>53</sup>	97, 58	87, 63
181	pavo.mut	<i>Pavo muticus</i> *	AF013763 <sup>53</sup>	97, 57	87, 63
182	tra.bly	<i>Tragopan blythii</i> *	AF200722 <sup>54</sup>	89, 55	85, 57
183	tra.sat	<i>Tragopan satyra</i> *	AF229837 <sup>54</sup>	89, 55	86, 61
184	tra.cob	<i>Tragopan caboti</i>	AF200723 <sup>54</sup>	89, 55	86, 61
185	tra.tem	<i>Tragopan temminckii</i> *	AF023802 <sup>55</sup>	89, 55	81, 56
186	arg.arg	<i>Argusianus argus</i>	AF013761 <sup>55</sup>	89, 55	87, 63
187	cat.wal	<i>Catrcus wallichi</i> *	AF023879 <sup>55</sup>	88, 54	85, 57

188 cro.cro	<i>Crossoptilon crossoptilon</i> *	AF018794 <sup>53</sup>	89, 55	85, 57
189 sym.ree	<i>Syrmaticus reevesi</i> *	AF018801 <sup>53</sup>	89, 55	85, 57
190 bam.tho	<i>Bambusicola thoracica</i> *	AF028790 <sup>53</sup>	80, 48	94, 64
191 fra.fra	<i>Francolinus francolinus</i>	AF013762 <sup>53</sup>	97, 58	86, 61
192 ith.cru	<i>Ithaginis cruentus</i> *	AF068193 <sup>53</sup>	98, 63	85, 57
193 ant.par	<i>Anthropoides paradisea</i>	U27557 <sup>56</sup>	85, 56	82, 58
194 ant.vir	<i>Anthropoides virgo</i>	U27545 <sup>56</sup>	84, 54	82, 52
195 gru.ant.an	<i>Grus antigone</i> <i>antigone</i>	U11060 <sup>57</sup>	90, 58	87, 63
196 gru.ant.gi	<i>Grus antigone</i> <i>gillae</i>	U11064 <sup>57</sup>	90, 58	87, 63
197 gru.any.sh	<i>Grus antigone</i> <i>sharpei</i>	U11061 <sup>57</sup>	90, 58	87, 63
198 gru.leu	<i>Grus leucogeranus</i> *	U27549 <sup>56</sup>	90, 58	87, 63
199 gru.can.pr	<i>Grus canadensis</i> <i>pratensis</i>	U27553 <sup>56</sup>	97, 60	87, 63
200 gru.can.ro	<i>Grus canadensis</i> <i>rowani</i>	U27552 <sup>56</sup>	97, 60	87, 63
201 gru.can.ta	<i>Grus canadensis</i> <i>tabida</i>	U27551 <sup>56</sup>	98, 63	87, 63
202 gru.can.ca	<i>Grus canadensis</i> <i>canadensis</i>	U27554 <sup>56</sup>	97, 61	87, 63
203 gru.ame	<i>Grus americana</i>	U27555 <sup>56</sup>	90, 58	87, 63
204 gru.gru	<i>Grus grus</i>	U27546 <sup>56</sup>	89, 54	87, 63
205 gru.mon	<i>Grus monacha</i> *	U27548 <sup>56</sup>	90, 58	87, 63
206 gru.nig	<i>Grus nigricollis</i> *	U27547 <sup>56</sup>	90, 58	87, 63
207 gru.jap	<i>Grus japonensis</i>	U27550 <sup>56</sup>	81, 54	87, 63
208 cic.boy	<i>Ciconia boyciana</i> *	NC_002196 <sup>58</sup>	94, 58	79, 60
209 rhe.ame	<i>Rhea americana</i>	AF090339 <sup>59</sup>	93, 63	79, 60
210 ant.alb	<i>Anthracoboceros albirostris</i> *	U89190 <sup>60</sup>	97, 61	86, 59
211 fal.fam	<i>Falco femoralis</i>	U83310 <sup>61</sup>	97, 61	86, 60
212 fal.ver	<i>Falco verpertinus</i>	U83311 <sup>61</sup>	97, 61	85, 57
213 fal.par	<i>Falco peregrinus</i> *	U83307 <sup>61</sup>	97, 61	84, 52
214 fal.spa	<i>Falco sparverius</i>	U83306 <sup>61</sup>	92, 59	80, 51
215 ayt.ame	<i>Aythya americana</i>	NC_000877 <sup>62</sup>	98, 63	94, 62
216 smi.sha	<i>Smithornis sharpei</i>	NC_000879 <sup>59</sup>	97, 58	90, 61
217 vid.cha	<i>Vidua chalybeata</i>	NC_000880 <sup>59</sup>	97, 60	87, 64
218 chry.pic	<i>Chrysemys picta</i>	NC_002073 <sup>63</sup>	89, 56	86, 57
219 emy.orb.ku	<i>Emys orbicularis</i>	AJ131425 <sup>64</sup>	90, 59	94, 63
220 che.mud	<i>Chelonia mydas</i> *	AB012104 <sup>65</sup>	90, 58	94, 63
221 eum.egt	<i>Eumeces egrelius</i>	AB016606 <sup>53</sup>	86, 55	73, 51

Table 1. Multiple sequence alignment of 471 bp fragment of mitochondrial cytochrome b gene of 221 animal species

cer.elo.xan	TACCATGAGGACAAATATCATTCTGAGGAGCAACGGTCATTACCAACCTCTCAGCAA	60
cer.elo.can	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCAGCAA	60
cer.nip.cent	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCAGCAA	60
cer.nip.yes	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCAGCAA	60
cer.nip.ker	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCAGCAA	60
cer.nip.pul	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCAGCAA	60
cer.nip.nip	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCAGCAA	60
cer.elo.sco	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCAGCAA	60
cer.dam	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAATCTCTCAGCAA	60
ran.tar	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAATCTCTCAGCAA	60
mos.fus	TACCTTGAGGACAAATATCATTCTGAGGAGCGACAGTTATTACCAATCTCTCAGCAA	60
mos.leu	TACCTTGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAATCTCTCAGCAA	60
mos.chr	TACCTTGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAATCTCTCAGCAA	60
mos.ber	TACCTTGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAATCTCTCAGCAA	60
mos.mos	TACCTTGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACTAACCTCTCAGCAA	60
tra.jav	TACCCCTGAGGACAGATACTTCTGAGGAGCCACAGTCATCACCAACCTTTATCAGCTA	60
trag.nap	TACCCCTGAGGGCAAAATATCTTTTGAGGAGCTACAGTCATCACTAACCTTTCTCAGCAA	60
bala.acu	TACCCCTGAGGACAAATATCATTTTGAGGTGCAACCGTCATCACCAACCTCTATCAGCAA	60
bala.bon	TACCCCTGAGGACAAATATCATTTTGAGGCCAACCGTCATCACCAACCTCTATCAGCAA	60
bala.bor	TACCCCTGAGGACAAATATCATTTTGAGGCCAACCGTCATCACCAACCTTTATCAGCAA	60
bala.edi	TACCCCTGAGGACAAATATCATTTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
esch.rob	TACCCCTGAGGACAAATATCATTCTGAGGGCGAACCGTTATCACCAACCTCTATCAGCAA	60
bala.mus	TGCCCTGAGGACAAATATCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
mega.nov	TACCCCTGAGGACAAATATCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
bala.phy	TGCCCTGAGGACAAATATCATTCTGAGGGCGAACACTGAAATCACCAACCTCTTATCAGCAA	60
cap.mar	TGCCCTGAGGACAGATACTCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
ceph.com	TACCCCTGGGGACAGATACTCATTCTGAGGGCGAACAGTCATCACCAACCTCTTATCAGCAA	60
ceph.eut	TACCCCTGGGGACAGATACTCATTCTGAGGGCGAACAGTCATCACCAACCTCTTATCAGCAA	60
lage.obl	TACCCCTGAGGACAAATATCATTCTGAGGGCGAACAGTCATCACCAACCTCTTATCAGCAA	60
ceph.hea	TACCCCTGAGGACAAATATCATTCTGAGGGCGAACAGTCATCACCAACCTCTTATCAGCAA	60
ceph.hec	TACCCCTGAGGACAAATATCATTCTGAGGGCGAACAGTCATCACCAACCTCTTATCAGCAA	60
lage.aus	TACCCCTGAGGACAGATACTCATTCTGAGGGCGAACAGTCATCACCAACCTCTTATCAGCAA	60
lage.cru	TACCCCTGAGGACAGATACTCATTCTGAGGGCGAACAGTCATCACCAACCTCTTATCAGCAA	60
lage.obs	TACCCCTGAGGGCGAGATACTCATTCTGAGGGCGAACAGTCATCACCAACCTCTTATCAGCAA	60
lisso.bor	TACCCCTGAGGACAGATACTCATTCTGAGGGCGAACAGTCATCACCAACCTCTTATCAGCAA	60
lisso.per	TACCCCTGAGGACAGATACTCATTCTGAGGGCGAACAGTCATCACCAACCTCTTATCAGCAA	60
glo.mac	TACCCCTGAGGACAGATACTCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
glo.mel	TACCCCTGAGGACAGATACTCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
fere.att	TACCCCTGAGGACAGATACTCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
pepo.ele	TACCCCTGAGGACAGATACTCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
gram.gri	TACCCCTGAGGACAAATATCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
pse.cra	TACCCCTGAGGACAGATACTCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
lage.acu	TACCATGAGGACAAATATCATTCTGAGGGCGAACCGTTATCACCAACCTCTTATCAGCAA	60
orti.bre	TACCCCTGAGGACAGATACTCATTCTGAGGGCGAACCGTCATTACTAATCTCTTATCAGCAA	60
crca.bre	TACCCCTGAGGACAGATACTCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
del.cap	TGCCCTGGGGACAAATATCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
del.tro	TGCCCTGAGGACAAATATCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
del.del	TGCCCTGAGGACAAATATCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
sten.cly	TGCCCTGAGGACAAATATCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
sten.coe	TGCCCTGAGGACAAATATCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
tur.adu	TGCCCTGAGGACAAATATCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
sten.fro	TGCCCTGAGGACAAATATCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
saus.chi	TGCCCTGAGGACAAATATCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
sten.lon	TACCCCTGAGGACAAATATCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
turs.tru	TGCCCTGAGGACAAATATCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
lage.alb	TACCCCTGAGGACAAATATCATTCTGAGGGCGAACCGTCATCACCAACCTCTTATCAGCAA	60
sten.bre	TACCCCTGAGGACAAATATCATTCTGAGGGCGAACCGTCATTACCAACCTCTTATCAGCAA	60
sota.flu	TACCCCTGAGGACAAATATCATTCTGAGGGCGAACCGTCATTACCAACCTCTTATCAGCAA	60

del.leu TACCCCTGAGGACAAATATCATTCTGAGGGCGAACCGTCATTACCAATCTCCTATCAGCAA 60  
 mono.mon TACCCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA 60  
 plac.gan TACCCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTTATCAGCAA 60  
 plac.min TACCCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTTATCAGCAA 60  
 kogi.bre TACCCCTGAGGCCAAATATCATTCTGAGGAGCAACCGTCATCACCAACCTTATCCGCAA 60  
 kogi.sim TGCCCTGAGGCCAAATATCATTCTGAGGAGCAACCGTCATCACCAACCTTATCCGCAA 60  
 phys.cat TGCCCTGAGGACAAATATCATTCTGAGGCCAACCGTTATCACCAACCTTATCAGCAA 60  
 lipo.vex TACCCCTGAGGACAAATATCATTCTGAGGCCAACCGTCATCACTAATCTTCTATCAGCAA 60  
 phoc.sin TGCCCTGGGGACAAATATCATTCTGAGGTGCTACCGTCATCACCAACCTTATCAGCAA 60  
 bera.bai TGCCTTGAGGGCAAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTTATCCGCTA 60  
 ziph.car TACCTTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTTATCCGCTA 60  
 meso.eur TTCCCTGAGGACAAATATCATTCTGAGGCCAACCGTTATTACCAACCTCCTATCCGCCA 60  
 meso.bid TACCCCTGAGGACAAATATCATTCTGAGGCCACTGTTATTACTAACCTCCTATCCGCTA 60  
 meso.den TACCATGAGGACAAATATCCTTCTGAGGTGCACTGTCATTACCAATCTCCTATCCGCTA 60  
 hype.amp TACCCCTGAGGACAAATATCATTCTGAGGCCAACCGTCATCACCAATCTCCTATCCGCTA 60  
 meso.per TACCTTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACTTATCAGCTA 60  
 pont.bla TACCCCTGAGGACAAATGTCATTCTGAGGGGCAACAGTCATCACCAACTTACTATCAGCTA 60  
 hex.lib TACCATGAGGACAAATATCATTCTGAGGGGCAACAGTCATCACCAACTTACTATCAGCTA 60  
 hipp.amp TGCCATGAGGACAAATGTCATTCTGAGGGGCAACAGTCATTACCAACTTACTGTCAAGCTA 60  
 dic.sum TACCATGAGGTCAAATATCCTTCTGAGGAGCCACAGTTATCACAATCTCCTCTCAGCCA 60  
 rhin.scn TACCATGAGGTCAAATATCCTTCTGAGGGGCTACAGTCATTACAAATCTCCTCTCAGCTA 60  
 cera TACCATGAGGCAAAATATCCTTCTGAGGGGCTACAGTCATCACCAACCTCCTATCAGCTA 60  
 equu TACCATGAGGACAAATATCCTTCTGAGGAGCAACGGTCATTACAAACCTCCTATCAGCTA 60  
 baby.bab TACCCCTGAGGACAAATATCATTCTGAGGGAGCTACCGTCATTACAAACCTACTATCAGCTA 60  
 phac.afr TACCATGAGGACAAATATCGTTCTGAGGAGCCACAGTCATCACCAACCTACTATCAGCTA 60  
 sus.bar TGCCTTGAGGACAAATATCATTCTGAGGGAGCTACGGTCATCACCAATCTACTATCAGCTA 60  
 sus.scr.ewb3 TGCCTTGAGGACAAATATCATTCTGAGGGAGCTACGGTCATCACCAATCTACTATCAGCTA 60  
 lama.gla .TCCCATGAGGACAAATATCATTCTGAGGGGCAACAGTAATTACAAATCTACTCTCGGCAA 60  
 lama.gua TCCCATGAGGCAAAATATCATTCTGAGGGGCAACAGTAATTACAAACCTACTCTCGGCAA 60  
 vic.vic TCCCATGAGGACAAATATCATTCTGAGGGGCAACAGTAATTACAAACCTACTCTCGGCAA 60  
 cam.bac TCCCATGAGGACAGATAATCATTCTGGGGAGCAACAGTAATTACCAACCTACTCTCGGCAA 60  
 arc.for TTCCCATGAGGACAAATATCATTCTGAGGGAGCGACCGTCATTACCAACCTCCTATCAGCAG 60  
 arc.gaz TTCCCATGAGGACAGATAATCATTCTGAGGGAGCAACCGTCATTACCAACCTCCTATCAGCAG 60  
 eum.jub TTCCGTGAGGACAAATATCATTCTGAGGGAGCAACCGTCATTACCAACCTCCTATCAGCAG 60  
 zal.cal TTCCCATGAGGACAAATATCATTCTGAGGGAGCAACCGTCATTACCAACCTCCTATCAGCAG 60  
 odo.ros TACCATGAGGACAAATATCCTTCTGAGGGAGCAACCGTCATCACCAACCTCTGTCAAGCTA 60  
 pho.fasciata TACCATGAGGACAAATATCATTCTGAGGGAGCAACAGTCATCACCAACTTACTATCAGCTA 60  
 pho.gro TACCATGAGGCAAAATGTCATTCTGAGGGAGCAACAGTCATTACAAATCTACTATCAGCTA 60  
 pho.vit TACCATGAGGACAAATATCATTCTGAGGGAGCAACAGTCATCACCAATCTACTATCAGCTA 60  
 cys.cri TACCATGAGGACAAATATCATTCTGAGGGAGCAACAGTCATCACCAACTTACTATCAGCTA 60  
 hyd.lep TACCATGAGGACAAATATCATTCTGAGGGAGCAACAGTCATTACCAACCTACTATCAGCTA 60  
 lep.wed TACCATGAGGACAAATATCATTCTGAGGGAGCAACAGTCATTACCAACCTACTATCAGCTA 60  
 mir.leo TGCCTTGAGGACAAATATCATTCTGAGGGAGCAACAGTCATTACCAACCTACTATCAGCTA 60  
 eri.bar TACCATGAGGACAAATATCATTCTGAGGGAGCAACAGTCATTACCAACCTACTATCAGCTA 60  
 mon.sch TACCCCTGAGGCCAAATATCCTTCTGAGGGAGCAACTGTCATTACCAATCTCTTATCAGCTA 60  
 hela.mal TACCCCTGAGGCCAAATATCCTTCTGAGGGAGCAACTGTCATTACCAACCTCCTATCAGCTA 60  
 sel.thi TACCCCTGAGGCCAAATATCCTTCTGAGGGAGCAACTGTCATTACCAACCTCCTATCAGCTA 60  
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 gla.sab TACCCCTGAGGACAGATAATCATTCTGAGGGAGCAACCGTTATCACCAACCTACTATCAGCTA 60  
 gla.vol TACCCCTGAGGACAAATATCCTTCTGAGGGAGCAACCGTAATCACAAACCTCCTGTCAAGCTA 60  
 hyl.pha TACCATGAGGCCAAATATCCTTCTGAGGGAGCAACCGTTATCACCAACCTACTATCAGCTA 60  
 pet.set TACCATGAGGCCAAATATCCTTCTGAGGGAGCAACCGTTATCACCAACCTACTATCAGCTA 60  
 bel.pea TACCATGAGGCCAAATATCCTTCTGAGGGAGCAACCGTTATCACCAACCTACTATCAGCTA 60  
 pte.mom TACCCCTGAGGCCAAATATCATTCTGAGGGAGCAACCGTTATCACCAACCTCCTATCCGCCA 60  
 gala.demi TTCCCATGAGGCCAAATATCATTCTGAGGGAGCAACCGTTATCACCAACCTCCTGTCAAGCTA 60

pero.pot	TCCCCATGAGGACAAATATCATTCTGAGGTGCCACAGTAATCACAACCTCTATCAGCAA	60
gala.mat	TCCCCATGAGGACAAATATCATTCTGAGGGGCCACCGTAATCACAACCTCTCTCAGCAA	60
gala.moh	TTCCCGTGAGGACAAATATCATTCTGAGGGGCCACCGTAATCACAACCTCTCTCAGCAA	60
oto.gar	TCCCCATGAGGACAAATATCATTCTGAGGGGCCACCGTAATTACAAATCTCTCTCAGCAA	60
loc.tar	TCCCCATGAGGACAAATATCATTCTGAGGGGCCACAGTAATTACCAACCTACTATCAGCAA	60
nyc.cou	TCCCCATGAGGACAAATATCATTCTGAGGTGCCACCGTCATCACAACCTACTATCAGCAA	60
mus	TTCCCATGAGGACAAATATCATTCTGAGGTGCCACAGTATTACAAACCTCTATCAGCAA	60
gorr	TCCCCATGAGGCCAAATATCCTCTGAGGGGCCACAGTAATCACAACCTGTCTATCAGCAA	60
homo	TCCCCGTGAGGCCAAATATCATTCTGAGGGGCCACAGTAATTACAAACCTACTATCAGCAA	60
dug.dug	TCCCCATGAGGACAAATATCATTCTGAGGGAGCAACCGTATTACTAACCTCTCTCAGCAA	60
ele.max	TTCCCATGAGGACAAATATCATTCTGAGGGGCCACCGTAATTACTAACCTCTCTCAGCAA	60
afr.con	TCCCCATGAGGCCAAATATCATTCTGAGGGGCCACGTCACTCACAAACCTATACTCAGCAA	60
pavo.mut	TCCCCATGAGGTCAAATGTCATTCTGAGGGGCCACGTATTACAAACCTATTCTCAGCAA	60
tra.bly	TCCCCATGAGGACAAATATCATTGAGGGGCTACCGTCATCACAAACCTATTCTCAGCAA	60
tra.sat	TCCCCATGAGGACAAATATCATTCTGAGGGGCCACGTCACTCACAAACCTATTCTCAGCAA	60
tra.cob	TCCCCATGAGGACAAATATCATTGAGGGGCCACGTATTACCAAAATCTATTCTCAGCAA	60
tra.tem	TCCCCATGAGGACAAATATCATTGAGGGGCCACGTATTACCAAAATCTATTCTCAGCAA	60
arg.arg	TCCCCATGAGGACAAATATCATTGAGGGGCCACGTATTACCAAAATCTATTCTCAGCAA	60
cat.wal	TTCCCATGGGGACAAATATCATTGAGGGGCCACGTATTACCAAAATCTATTCTCAGCAA	60
cro.cro	TCCCCATGAGGACAAATATCATTGAGGGGCCACGTATTACCAAAATCTATTCTCAGCAA	60
sym.ree	TCCCCATGAGGACAAATATCATTGAGGGGCCACGTATTACCAAAATCTATTCTCAGCAA	60
bam.tho	TCCCCATGGGGCCAATATCCTTTGAGGGGCCACGTATTACCAAAATCTATTCTCAGCAA	60
fra.fra	TCCCCATGAGGCCAAATATCATTCTGAGGGGCCACGTATTACCAAAATCTATTCTCAGCAA	60
ith.cru	TACCATGAGGACAAATATCATTCTGAGGGGCCACGTATTACCAAAACCTACTCTCAGCAA	60
ant.par	TACCATGAGGACAAATATCATTGAGGGGCCACGTATTACCAAAATCTATTCTCAGCAA	60
ant.vir	TACCATGAGGACAAATGTCATTGAGGGGCCACGTATTACCAAAATCTCTTCTCAGGCCG	60
gru.ant.ant	TACCATGGGGACAAATGTCATTGAGGGGCCACGTATTACCAAAATCTCTTCTCAGGCCG	60
gru.ant.gil	TACCATGAGGACAAATATCATTGAGGGGCCACGTATTACCAAAATCTCTTCTCAGGCCG	60
gru.ant.sha	TACCATGAGGACAAATATCATTGAGGGGCCACGTATTACCAAAATCTCTTCTCAGGCCG	60
gru.leu	TACCATGAGGACAAATATCATTGAGGGGCCACGTATTACCAAAATCTCTTCTCAGGCCG	60
gru.can.pra	TGCCCCATGAGGACAAATATCATTCTGAGGGGCCACGTATTACCAAAACCTCTTCTCAGGCCG	60
gru.can.row	TACCATGAGGACAAATATCATTCTGAGGGGCCACGTATTACCAAAACCTCTTCTCAGGCCG	60
gru.can.tab	TACCATGAGGACAAATATCATTCTGAGGGGCCACGTATTACCAAAACCTCTTCTCAGGCCG	60
gru.can.can	TACCATGAGGACAAATATCATTCTGAGGGGCCACGTATTACCAAAACCTCTTCTCAGGCCG	60
gru.ame	TACCATGGGGACAAATGTCATTGAGGGGCCACGTATTACCAAAACCTCTTCTCAGGCCG	60
gru.gru	TACCATGAGGACAAATATCATTGAGGGGCCACGTATTACCAAAACCTCTTCTCAGGCCG	60
gru.mon	TACCATGAGGACAAATATCATTGAGGGGCCACGTATTACCAAAACCTCTTCTCAGGCCG	60
gru.nig	TACCATGAGGACAAATATCATTGAGGGGCCACGTATTACCAAAACCTCTTCTCAGGCCG	60
gru.jap	TGCCCCATGAGGACAGATATCATTCTGAGGGGCCACGTATTACCAAAACCTATTCTCAGCTA	60
cic.boy	TACCATGAGGACAAATATCATTCTGAGGGGCCACGTATTACCAAAACCTATTCTCAGCTA	60
rhe.ame	TACCATGAGGACAAATATCATTCTGAGGGGCCACGTATTACCAAAACCTATTCTCAGCTA	60
ant.alb	TACCATGAGGACAAATATCATTCTGAGGGGCCACGTATTACCAAAACCTATTCTCAGCTA	60
fal.fam	TACCATCTGAGGACAAATATCATTCTGAGGGGCCACGTATTACCAAAACCTATTCTCAGCTA	60
fal.ver	TACCATCTGAGGACAAATATCATTCTGAGGGGCCACGTATTACCAAAACCTATTCTCAGCTA	60
fal.per	TACCATCTGAGGACAAATATCATTCTGAGGGGCCACGTATTACCAAAACCTATTCTCAGCTA	60
fal.spa	TACCATGAGGACAAATATCATTCTGAGGGGCCACGTATTACCAAAACCTATTCTCAGCTA	60
ayt.ame	TACCATGAGGACAAATATCATTCTGAGGGGCCACGTATTACCAAAACCTATTCTCAGCTA	60
smi.sha	TCCCCATGAGGCCAAATATCATTCTGAGGTGCCACAGTAATCAGCAAACCTCTTCTCAGCTA	60
vid.cha	TGCCCCATGAGGACAAATATCATTCTGAGGTGCCACAGTAATCAGCAAACCTCTTCTCAGCTA	60
chry.pic	TACCATGGGGCCAATATCCTCTGAGGTGCCACCGTTATTACTAACCTCTTCTCAGGCCG	60
emy.orb.kuz	TACCATGGGGCCAATATCCTCTGAGGTGCCACCGTTATTACTAACCTCTTCTCAGGCCG	60
che.mud	TACCATGAGGACAAATATCATTGAGGGGCCACCGTTATTACTAACCTACTCTCAGGCCG	60
eum.egr	TCCCCATGGGGACAGATATCCTCTGAGGGGCCACCGTTATTACTAACCTACTCTCAGGCCG	60
	*** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** ***	
sep.mel	TCCCCATACATTGCTACAAACCTACTAGAATGAAATCTGAGGTGCCACAGTAATCAGCAAAG	120
pre.ore	TTCCCATATATTCGGCACAAACCTGCTAGAATTAAATCTGAGGTGCCACCGTTATTACTAACCTCTTCTCAGGCCAAG	120
adi.nas	TCCCCATATATCGGCACAGACCTTCTGAGGTGCCACCGTTATTACTAACCTCTTCTCAGGCCAAG	120

ory.dam	TCCCATAACATCGGCACAAAATCTAGTCGAATGAAATTGAGGGGGATTCTCCGTAGACAAAG	120
hip.equ	TCCCATAATATTGGCACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCCGTAGACAAAG	120
alc.bus	TCCCATAATATTGGCACACAGACCTAGTAGAAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
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bea.hun	TTCCATAATATTGGTACAAAACCTAGTCGAATGAAATCTGAGGGGGCTTCTCACTAGACAAAG	120
dam.lun	TTCCATAACATCGGCACAAAATCTAGTCGAATGGATCTGAGGGGGCTTCTCACTAGACAAAG	120
con.tau	TCCCATAACATTGGCACTAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
amm.les	TCCCATAATATTGGCACAAAATCTAGTCGAATGGATCTGAGGGGGATTCTCACTAGACAAAG	120
pse.ray	TCCCATAATATTGGCACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
cap.ibe	TCCCATAATATTGGCACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
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cap.fal	TCCCATAACATTGGCATAGACTTAGTCGAGTGAATCTGAGGGGGCTTCTCGGTAGACAAAG	120
rup.pyt	TCCCATAATATTGGCACACAGACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
rup.rup	TCCCATAATATTGGCACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
nem.cau	TCCCATAATATTGGCACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
bud.tax.tax	TCCCATAACATTGGCACACAGACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
pan.hod	TCCCATAATATTGGCACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
ovi.amm	TCCCATAATATTGGCACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
ovi.vig	TCCCATAATATTGGCACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCCGTAGACAAAG	120
cap.cri	TCCCATAATATTGGCACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCCGTAGACAAAG	120
ovi.mos	TCCCATAACATCGGCACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
ore.ame	TCCCATAACATCGGTACAGACCTAGTCGAATGAAATCTGAGGGGGCTTCTCACTAGACAAAG	120
cep.dor	TCCCATAACATTGGTACAAAACCTAGTCGAATGAAATCTGAGGGGGCTTCTCACTAGACAAAG	120
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bos.tta	TCCCATAACATTGGCACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
bub.min	TCCCATAACATTGGTACAAGTCTGGTTGAATGAAATTGAGGGGGATTCTCACTAGACAAAG	120
buba.bub	TCCCATAATATTGGCACACAAAACCTAGTCGAATGAAATCTGAGGGGGCTTCTCGGTAGACAAAG	120
tra.ang	TCCCATAATATTGGCACACACCTAGTCGAATGAAATCTGAGGGGGCTTCTCACTAGACAAAG	120
tra.eur	TCCCATAATATTGGCACACACCTAGTCGAATGAAATCTGAGGGGGCTTCTCACTAGACAAAG	120
kob.ell	TCCCATAACATTGGCACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
kob.mes	TCCCATAATATTGGCACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
red.aru	TCCCATAACATCGGCACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
red.sul	TCCCATAACATCGGCACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
neo.mos	TCCCATAATATTGGCACACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
pel.cap	TCCCATAACATTGGTACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
gaz.dam	TCCCATAACATCGGCACACAGACCTAGTAGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
our.out	TCCCATAACATTGGTACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
ant.cer	TCCCATAACATCGGTACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
sai.tat	TCCCATAATATTGGCACACAGACCTAGTAGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
mad.kir	TCCCATAATATTGGCACACAAAACCTAGTCGAATGAAATCTGAGGGGGCTTCTCACTAGACAAAG	120
rap.mel	TCCCATAATATTGGCACACACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
gaz.gaz	TCCCATAACATCGGCACACAAAACCTAGTAGAATGAAATCTGAGGGGGATTCTCGGTAGACAAAG	120
ant.ame	TCCCATAACATTGGTACTAACCTAGTAGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
hyd.lne	TCCCATAACATTGGTACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
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ces.elia.kan	TCCCATAACATTGGCACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
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ces.nip.nip	TCCCATAATATTGGCACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
ces.elia.opp	TCCCATAACATTGGCACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120
ces.dam	TCCCATAATATTGGCACACAAAACCTAGTCGAATGAAATCTGAGGGGGATTCTCACTAGACAAAG	120

ran.car	TTCCATATATTGGTACAAATCTAGTCGAACTGAATTTCAGGAGGATTTCTGTAGATAAAG	120
mos.fus	TTCCATACATTGGTACTAATCTGGTTGAATGAATTTCAGGAGGCTTCTCACTAGACAAAG	120
mos.leu	TTCCATACATTGGTACTAATCTGGTTGAATGAATTTCAGGAGGCTTCTCACTAGACAAAG	120
mos.chr	TTCCATACATTGGTACTAACCTGGTTGAATGAATTTCAGGAGGCTTCTCACTAGACAAAG	120
mos.ber	TTCCATACATTGGTACTAATCTGGTTGAATGAATCTGAGGAGGCTTCTCACTAGACAAAG	120
mcs.mos	TTCCCATACATTGGTACTAACCTGGTTGAAGTGAAATTTCAGGAGGCTTCTCACTAGACAAAG	120
tra.jav	TCCCATACATTGGCAGAGCTTGGTCAATGAATCTGAGGCGGTTCTCACTAGACAAAG	120
trag.nap	TCCCCTATATCGGCACCGAACTAGTTGAATGAATCTGAGGCGGTTCTCACTAGACAAAG	120
bala.acu	TCCCATACATTGGTACCAACCTTAGTTGAATGAATCTGAGGCGGCTTCTGTAGACAAAG	120
bala.bon	TCCCATACATTGGTACTACCCTAGTCGAATGAATCTGAGGCGGTTCTGTAGACAAAG	120
bala.bor	TCCCATACATTGGTACTACCCTAGTCGAATGAATCTGGGGCGGTTCTGTAGACAAAG	120
bala.edi	TCCCATACATTGGCAGACTACCCCTAGTCGAATGGGTCTGAGGCGGTTCTGTAGACAAAG	120
esch.rob	TCCCATACATTGGTACTACCCTAGTCGAATGAATCTGAGGCGGTTCTGTGGATAAAG	120
bala.mus	TCCCATACATTGGTACTACCCTAGTCGAATGAATCTGGGGCGGTTCTGTAGACAAAG	120
mega.nov	TCCCATACATTGGTACCAACCTAGTTGAATGAATCTGAGGCGGTTCTGTAGACAAAG	120
bala.phy	TCCCATACATTGGTACTACCCTAGTCGAATGAATCTGGGGCGGTTCTGTAGACAAAG	120
cap.mar	TCCCCTACATCGGTACTACCCCTAGTCGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
ceph.com	TCCCCTACATCGGTACTACCCCTAGTCGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
ceph.eut	TCCCCTACATCGGTACTACCCCTAGTCGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
lage.obl	TCCCCTACATCGGTACTACCCCTAGTCGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
ceph.hea	TCCCCTACATCGGTACTACCCCTAGTCGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
ceph.hec	TCCCCTACATCGGTACTACCCCTAGTCGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
lage.aus	TCCCCTACATCGGTACTACCCCTAGTCGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
lage.cru	TCCCCTACATCGGTACTACCCCTAGTCGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
lage.obs	TCCCCTACATCGGTACTACCCCTAGTCGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
lisso.bor	TCCCCTACATCGGTACTACCCCTAGTCGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
lisso.per	TCCCCTACATCGGTACTACCCCTAGTCGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
glo.mac	TCCCCTACATCGGCACCAACCTAGTCGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
glo.mel	TCCCCTACATCGGCACCAACCTAGTCGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
fere.att	TCCCCTACATCGGAACCAACCTAGTCGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
pepo.ele	TCCCCTACATCGGTACTACCCCTAGTCGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
gram.gri	TCCCCTACATCGGTACCACTTAGTCGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
pse.cra	TCCCCTACATCGGCACCAACCTAGTCGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
lage.acu	TCCCCTACATCGGCACCAACCTAGTCGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
orc1.bre	TCCCCTACATCGGCACCAACCTAGTCGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
orca.bre	TCCCCTATATTGGCACTACCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
del.cap	TCCCCTATATTGGCACTACCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
del.tro	TCCCCTATATTGGCACTACCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
del.del	TCCCCTATATTGGCACTACCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
sten.cly	TCCCCTATATTGGCACTACCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
sten.coe	TCCCCTATATTGGCACTACCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
tur.adu	TCCCCTATATTGGCACTACCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
sten.fro	TCCCCTATATTGGCACTACCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
saus.chi	TCCCCTATATTGGCACTACCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
sten.lon	TCCCCTATATTGGCACTACCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
turs.tru	TCCCCTATATTGGCACTACCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
lage.alb	TCCCCTACATCGGCACCAACCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
sten.bre	TCCCCTACATCGGCACCAACCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
sota.flu	TCCCCTACATCGGCACCAACCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
del.leu	TCCCCTACATCGGCACCAACCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
mono.mon	TCCCCTATATTGGCACTACCCCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
plat.gan	TCCCCTATATTGGCACTACCCCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
plat.min	TCCCCTATATTGGCACTACCCCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
kogi.bre	TCCCCTACATCGGCACCAACCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
kogi.sim	TCCCCTACATCGGCACCAACCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
phys.cui	TCCCCTACATCGGCACCAACCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
lipo.wek	TCCCCTACATCGGCACCAACCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120
phoc.sin	TCCCCTACATCGGCACCAACCTAGTCGAATGAATCTGAGGCGGATTCTCGTAGACAAAG	120

bera.bai	TTCCTTATATCGGCACCACTCTTGCGAATGAATCTGAGGTGGCTTCTCCGTAGATAAAAG	111
ziph.cat	TCCCCCTATATCGGCACTACTCTAGTCGAATGAATCTGAGGTGGCTTCTCCGTAGATAAAAG	112
meso.eur	TCCCCCTATATTGGCACTACTCTAGTCGAATGAATCTGAGGTGGCTTCTCCGTAGATAAAAG	113
meso.bid	TTCCCCTACATCGGCACCACTACCCCTAGTTGAATGAATCTGAGGTGGCTTCTCCGTAGACAAG	113
meso.den	TTCCCCTATATTGGCACCCACCCCTAGTTGAATGAATCTGAGGTGGCTTCTCCGTAGATAAAAG	113
hyde.amp	TTCCCCTATATCGGCACTAACCCCTAGTTGAATGAATCTGAGGTGGCTTCTCCGTAGATAAAAG	113
meso.per	TCCCCTTATATTGGCACCCACCCCTAGTTGAATGAATTTCAGGTGGCTTCTCCGTAGATAAAAG	113
ponc.bla	TCCCCTACATCGGCACCTACCCCTAGAATGGATCTGAGGTGGCTTCTCCGTAGACAAG	113
hex.lib	TCCCCTACATGGAACAGACCTAGTAGAATGAATCTGAGGTGGCTTCTCCGTAGACAAG	113
hipp.amp	TCCCCTATATTGGAACAGACCTAGTAGAATGAATCTGAGGTGGCTTCTCCGTAGACAAG	113
dic.sum	TCCCCTACATCGGCACCGACCTTGAGAATGAATCTGAGGGGGATTCTCCGTAGACAAG	113
rhin.son	TCCCCTATATCGGTACCAACCTTGAGAATGAATCTGAGGGAGGATTCTCGACACAAG	113
cera	TCCCCTACATCGGCACCAACCTCGTAGAATGAATCTGAGGGAGGATTCTCGACACAAG	113
equu	TCCCCTACATCGGTACTACGCTCGTAGAATGAATCTGAGGTGGATTCTCAGTAGACAAG	113
baby.bab	TCCCCTATATCGGAACGGACCTCGTAGAATGGATCTGAGGGAGGCTTCTCCGTAGATAAG	113
phac.afr	TCCCCTACATGGAACAAATCTTGAGAATGAATCTGAGGGAGGTTCTCCGTAGACAAG	113
sus.bar	TCCCCTATATCGGAACAGACCTCGTAGAATGAATCTGAGGGGGCTTCTCCGTAGACAAG	113
sus.scr.ewb3	TCCCCTATATCGGAACAGACCTCGTAGAATGAATCTGAGGGGGCTTCTCCGTAGACAAG	113
lama.gla	TCCCCTATATCGGAACAGACACTAGTCGAATGAATTTGAGGGGGTTCTCCGTAGATAAG	113
lama.gua	TTCCCATACGTTGGTACACACTAGTCGAGTGGATTTGAGGGAGGATTCTCCGTAGATAAG	113
vic.vic	TTCCCCTATATCGGCACACACTAGTAGAATGAATTTGAGGTGGCTTCTCCGTAGACAAG	113
cam.bac	TTCCCCTACATGGGACCCACCTAGTAGAATGAATTCTGAGGGAGGATTCTGAGTAAAG	113
arc.for	TCCCCTACATCGGAACAACTAGTAGAATGAATTCTGAGGGAGGATTCTGAGTAAAG	113
arc.gaz	TCCCCTACATCGGAACCAACTAGTAGAATGAATTCTGAGGGGGATTCTAGTCGACACAAG	113
eum.jub	TCCCCTACATCGGAACCCRACCTAGTAGAATGAATTCTGAGGGGGATTCTAGTCGACACAAG	113
sal.cal	TCCCCTATGTAGGGACTGACTTGCTCGAATGAGTCAGGGGGTTCTAGTTGATTAAG	113
odo.ros	TCCCCTATATCGGAACCGACCTAGTAGAATGAATTCTGAGGGAGGATTCTAGTTGATTAAG	113
pho.fasciata	TCCCCTACATCGGAACCGATCTAGTAGAATGAATTCTGAGGGAGGTTCTAGTTGATTAAG	113
pho.gro	TCCCCTACATCGGAACCGATCTAGTAGAATGAATTCTGAGGGAGGTTCTAGTTGATTAAG	113
pho.vit	TCCCCTATGTGGAAACCGACCTTGAGAATGAATTCTGAGGGAGGTTCTAGTTGATTAAG	113
cys.cri	TCCCCTACATCGGAGCCGATCTAGTAGAATGAATTCTGAGGGGGATTCTAGTTGATTAAG	113
hyd.lep	TCCCCTACATCGGAACCGACCTAGTAGAATGAATTCTGAGGGGGATTCTAGTTGATTAAG	113
lep.wed	TCCCCTACATCGGAGACCGACCTAGTAGAATGAATTCTGAGGGGGATTCTAGTTGATTAAG	113
mir.les	TCCCCTATGTGGAGACCGACCTAGTAGAATGAATTCTGAGGGGGATTCTAGTTGATTAAG	113
eri.bar	TCCCCTACATCGGGACTGATCTAGTAGAATGAATTCTGAGGGGGATTCTAGTTGATTAAG	113
mon.sch	TCCCCTACATCGGAACCGATCTAGTAGAATGAATTCTGAGGGGGATTCTAGTTGATTAAG	113
hela.mal	TCCCCTATATTGGAACCGACCTAGTAGAATGAATTCTGAGGGGGATTCTAGTTGATTAAG	113
sel.chi	TCCCCTATATTGGAACAGACCTAGTAGAATGAATTCTGAGGGGGATTCTAGTTGACACAAG	113
ail.ful	TTCCCCTATATTGGAACTAACCTTGAGTGAATCTGAGGGGGTTCTCAGTAGACAAG	113
fel	TTCCCATACATCGGAACCTGACTAGTAGAATGAATCTGAGGGGGTTCTCAGTAGACAAG	113
can	TCCCCTATATCGGAACCTGACTAGTAGAATGGATCTGAGGGGGCTTCTCAGTAGACAAG	113
tal	TTCCCCTACATCGGTACAGACCTAGTAGAATGAATTTGAGGTGGTTCTCAGTAGACAAG	113
gla.sab	TTCCCCTATATTGGACACACCTTGAGAATGAATCTGAGGGGGCTTCTCAGTAGACAAG	113
gla.vol	TTCCCCTATATTGGACACACCTTGAGAATGAATCTGAGGGGGATTCTCAGTAGACAAG	113
hyl.pha	TCCCCTACATGGAACACGCTTGTGAAATGAATTGGAGGGGATTCTCAGTAGACAAG	113
pet.see	TCCCCTATATTGGAACACGCTTGTGAAATGAATTGGAGGGGATTCTCAGTAGACAAG	113
bel.pea	TCCCCTATATTGGAACACGCTTGTGAAATGAATTGGAGGGGATTCTCAGTAGACAAG	113
pse.mom	TCCCCTATATTGGACACCAACCTTGAGAATGAATCTGAGGGGGATTCTCAGTAGACAAG	113
gala.demi	TCCCCTATATTGGACACCAACCTTGAGAATGAATCTGAGGGGGATTCTCAGTAGACAAG	113
pero.pot	TCCCCTATATTGGACACCAACCTTGAGAATGAATCTGAGGGGGATTCTCAGTAGACAAG	113
gala.mat	TCCCCTACATGGGACCTGCTAGTAGAATGAATCTGAGGGGGATTCTCAGTAGACAAG	113
gala.mch	TCCCCTATATTGGACACCAACCTTGAGAATGAATCTGAGGGGGATTCTCAGTAGACAAG	113
cto.gar	TCCCCTACATGGGACACCAACCTTGAGAATGAATCTGAGGGGGATTCTCAGTAGACAAG	113
loc.eas	TCCCCTACATGGGACACCAACCTTGAGAATGAATCTGAGGGGGATTCTCAGTAGACAAG	113
nyc.con	TCCCCTATATTGGACACCAACCTTGAGAATGAATCTGAGGGGGATTCTCAGTAGACAAG	113
mus	TCCCCTACATGGGACACCAACCTTGAGAATGAATCTGAGGGGGATTCTCAGTAGACAAG	113
gira	TCCCCTACATGGGACACCAACCTTGAGAATGAATCTGAGGGGGATTCTCAGTAGACAAG	113
homo	TCCCCTACATGGGACACCAACCTTGAGAATGAATCTGAGGGGGATTCTCAGTAGACAAG	113

dug.dug	TCCCCCTACATCGGCACCAACCTAGTCGAATGAGTTGACGGGGATTCTCAGTAGACAAAG	119
ele.max	TTCCCTACATCGGCACAAACCTAGTAGAATGAAATTGAGGAGGTTTCTGGTAGATAAAC	120
afr.con	TCCCCCTATATTGGCTAAACCCCTAGTAGAATGGGCTGAGGAGGATTCTCAGTTGACAACC	120
pavo.mut	TCCCCCTATATTGGCACAAACCCCTAGTAGAATGACCTGACGGGGATTCTCAGTCAGAAC	120
tra.bly	TCCCATAACATTGGCCTAAACCCCTAGTAGAATGAGCCTGAGGAGGTTTCTAGTTGACAATC	120
tra.sat	TCCCATAACATTGGCTAAACCCCTAGTAGAATGAGCCTGAGGAGGTTTCTAGTTGACAATC	120
tra.cob	TCCCATAACATTGGCCTAAACCCCTAGTAGAATGAGCCTGAGGAGGTTTCTAGTTGACAATC	120
tra.tem	TCCCATAACATTGGCCTAAACCCCTAGTAGAATGAGCCTGAGGAGGTTTCTAGTTGACAATC	120
arg.arg	TCCCCCTATATTGGCACAAACCCCTAGTAGAGTGAGGCTGAGGAGGATTCTCAGTTGACAATC	120
cat.wal	TCCCCCTACATCGGAGAGACCCCTAGTAGAATGACCTGAGGAGGATTCTCAGTTGACAATC	120
cro.cro	TCCCCCTACATCGGCCTAAACCCCTAGTAGCAGTCAGGCTGAGGGGGATTCTCAGTTGACAATC	120
sym.ree	TCCCCCTACATCGGCCTAAACCCCTAGTAGACTGGGCTGAGGAGGATTCTCAGTTGACAATC	120
bam.tho	TTCCCCCTACATCGGACAAACCCCTAGTAGAATGACCTGGGGGGATTCTCAGTAGACAACC	120
fra.fra	TTCCCCCTACATCGGACAAACCCCTAGTAGAGTGAGGCTGAGGAGGATTCTCAGTAGATAACC	120
ith.cru	TTCCCCCTACATCGGACAAACCCCTAGTAGAGTGAGGCTGAGGAGGATTCTCAGTAGATAACC	120
ant.par	TCCCCCTACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGTTTCTCAGTAGATAATC	120
ant.vir	TCCCCCTACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGTTTCTCAGTAGACAATC	120
gru.ant.ant	TCCCCCTACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
gru.ant.gil	TCCCCCTACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
gru.ant.sha	TCCCCCTACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
gru.leu	TCCCCCTACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
gru.can.pra	TCCCCCTACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
gru.can.row	TCCCCCTACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
gru.can.tab	TCCCCCTACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
gru.can.can	TCCCCCTACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
gru.ame	TCCCCCTACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
gru.gru	TCCCCCTACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
gru.mon	TCCCCCTACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
gru.nig	TCCCCCTACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
gru.jap	TCCCCCTACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
cic.boy	TCCCCCTACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
the.ame	TCCCCGTACATCGGACAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
ant.alb	TCCCCCATACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
fal.fam	TCCCCCATACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
fal.ver	TCCCCCATACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
fal.per	TCCCCCATACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
fal.spa	TCCCCCATATATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
ayt.ame	TCCCCCATACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
smi.sha	TTCCCCCATACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
vid.cha	TTCCCCCATACATCGGCCTAAACCCCTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
chry.pic	TCCCCATTACATTGGTAACACATTAGTAGAATGAGCCTGAGGGGGCTTCTCAGTAGACAATC	120
ewy.oob.kur	TCCCCATAACATTGGCAATACACTAGTCGAATGAACTGAGGGGGCTTCTCAGTAGACAATC	120
che.mud	TCCCCATAACATCGGCCTAAACCCCTAGTAGAATGAACTGAGGGGGCTTCTCAGTAGACAATC	120
eum.egg	TTCCCCCATACATCGGCCTAAACCCCTAGTAGAATGAACTGAGGGGGCTTCTCAGTAGACAATC	120
* * * * *		
aep.mel	CAACCCCTNACCGGATTTTCTGCTTTCACCTTCATGTTGATTCATTCATTCGGGACTAG	130
ore.oce	CAACCCCTTACCGGATTTTCTGCTTTCATGTTGATTTTCATTCATTCGGGACTAG	130
add.nas	CAACCCCTTACCGGATTTTCTGCTTTCATGTTGATTTTCATTCATTCGGGACTAG	130
cty.dam	CAACCCCTTACCGGATTTTCTGCTTTCATGTTGATTTTCATTCATTCGGGACTAG	130
hip.equ	CAACCCCTTACCGGATTTTCTGCTTTCATGTTGATTTTCATTCATTCGGGACTAG	130
alc.bus	CAACCCCTTACCGGATTTTCTGCTTTCATGTTGATTTTCATTCATTCGGGACTAG	130
sig.lit	CAACCCCTTACCGGATTTTCTGCTTTCATGTTGATTTTCATTCATTCGGGACTAG	130
bea.bun	CAACCCCTTACCGGATTTTCTGCTTTCATGTTGATTTTCATTCATTCGGGACTAG	130
dim.lun	CAACCCCTTACCGGATTTTCTGCTTTCATGTTGATTTTCATTCATTCGGGACTAG	130
con.tan	CAACCCCTTACCGGATTTTCTGCTTTCATGTTGATTTTCATTCATTCGGGACTAG	130
imm.lee	CTACTCTACCGGATTTTCTGCTTTCATGTTGATTTTCATTCATTCGGGACTAG	130
sue.nay	CCACTCTACCGGATTTTCTGCTTTCATGTTGATTTTCATTCATTCGGGACTAG	130

cap.ibe	CCACTCTCACCGGATTCTTCCCTTCACTTCATCTCCATTTCATCATCATTACAGCCCTCG	180
hem.jem	CTACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
cap.fal	CCACCCCTACCCGGATTCTTCCGCTTCCACTTTATCTCCATTTCATCATGCAGCCCTCG	180
rup.pyr	CTACCCCTACCCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
rup.rup	CTACCCCTACCCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
nem.cau	CTACTCTACCCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATACAGCTCTCG	180
bud.tax.tax	CATCCCTCACCCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCCAGACCTCG	180
pan.hod	CTACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
ovi.amm	CCACCCCTACCCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
ovi.vig	CCACCCCTACCCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATCACAGCCCTCG	180
cap.cri	CCACCCCTACCCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATCGTAGCCCTCG	180
ovi.mos	CCACCCCTACCCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
ore.ame	CTACCCCTACCCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
cep.dor	CAACTCTACCCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
cep.max	CAACCCCTACTCGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATACCAATTG	180
bis.bon	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATCGCAATTG	180
bos.gru	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
bos.zra	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
bub.min	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
buba.bub	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATACAGCGCTCG	180
tra.ang	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATACAGCCTAG	180
tra.eur	CAACCTTAACCCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCGCGGCTATTA	180
kob.ell	CAACCCCTAACCGGTTCTTCCGCTTCCACTTCATCTCCATTTCATCATCGCTATCG	180
kob.meg	CAACCCCTAACCGGTTCTTCCGCTTCCACTTCATCTCCATTTCATCATCGAGCTCTCG	180
red.aru	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATAGCCCTCG	180
red.ful	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATCGAGCCTCG	180
neo.mos	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
pel.cap	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATCGAGCCCTCG	180
gaz.dam	CAACACTCACCCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
our.our	CAACACTCACCCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
ant.cer	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
sai.tat	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
mad.kir	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
rap.mel	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
gaz.gaz	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
anti.ame	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
hyd.ine	CTACCCCTGACCCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCTCTCG	180
mun.mun	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
alc.alc	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
cer.elia.kan	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
cer.elia.xan	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
cer.elia.can	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
cer.nip.cent	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
cer.nip.yes	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
cer.nip.ket	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
cer.nip.pul	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
cer.nip.nip	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
cer.elia.sca	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
cer.dam	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
san.tar	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
mos.fus	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
mos.leu	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
mos.sch	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
mos.bes	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
mos.mos	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
tra.jav	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
tra.gn	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180
cal.lutu	CAACCCCTAACCGGATTCTTCCGCTTCCACTTCATCTCCATTTCATCATGCAGCCCTCG	180

bala.bon	CAACATTAAACACGGTTTTCGCTTCCACTTCATCCTCCCTTCATTATCCTAGCATTAG	180
bala.bor	CAACACTAACACGGTTTTCGCTTCCACTTCATTCTCCCTCATTATCCTAGCATTAG	180
bala.edi	CAACACTAACACGGTTTTCGCTTCCACTTCATTCTCCCTCATTATCCTAGCATTAG	180
esch.rob	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTATCCTAGCATTAG	180
bala.mus	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCCTCATTCAATTATCCTAGCATTAG	180
mega.nov	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCCTCATTCAATTACAGGATTAG	180
bala.phy	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCCTCATTATCCTAGCATTAG	180
cap.mas	CGACACTAACCTGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
ceph.com	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
ceph.euc	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
lage.obl	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
ceph.hea	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
ceph.hec	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAA	180
lage.aus	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
lage.cru	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
lage.cbs	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
lisso.bor	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
lisso.per	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
glo.mac	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
glo.mel	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
fera.att	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
pepo.ele	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
gram.gri	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAA	180
pse.cra	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTACAGGATTAG	180
lage.acu	CAACACTGACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAA	180
crcl.bre	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
orca.bre	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
del.cap	CAACATTAAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
del.zro	CAACATTAAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
del.del	CAACATTAAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
sten.cly	CAACATTAAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
sten.coe	CAACATTAAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
tur.adu	CAACATTAAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
sten.fro	CAACATTAAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
saus.chi	CAACATTAAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
sten.lon	CAACATTAAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
turs.bru	CAACATTAAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
lage.alb	CAACATTAAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
sten.bre	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
sota.flu	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
del.leu	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
mono.mon	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
plat.gan	CAACACTAACACGGATTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
plaz.mia	CAACACTAACACGGATTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
kogi.bre	CAACACTAACACGGATTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
kogi.sim	CCACATTAAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
phys.cat	CTACGCTTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAA	180
lipo.yek	CAACACTGACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAA	180
phoc.sin	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAA	180
bera.bat	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
ziph.gig	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
meso.sur	CTACGCTTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
meso.bid	CCACATTAAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
meso.den	CTACGCTTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
cype.imp	CTACGCTTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
meso.pcc	CTACGCTTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
peant.bla	CAACACTAACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180
hex.lib	CAACCTTACACGGTTTTCGCTTCCACTTCATCCTCCATTCAATTCAACAGGATTAG	180

hipp.amp	CCACCCCTAACACGATTCTTGCCTTCCACTTTATCCTTCCATTGCTTATCACAGCACTAG	180
dic.sum	CCACCCCTAACCGGTTCTTGCCTTCCACTTCATCCTCCCTCATCATCTAGCCCTAG	180
rhin.son	CTACCCCTAACCGATTCTTGCCTTCCACTTCATCCTCCCTTATTATCTAGCTCTAG	180
cera	CCACACTTACACGATTCTTGCCTTCCACTTATCCTCCCTTATTATCATAGCCCTAG	180
equu	CCACCCCTAACCGATTCTTGCCTTCCACTTTATCCTACCCCTTATCATCATCAGCCCTGG	180
baby.bab	CAACCCCTAACACGATTCTTGCCTTCCACTTTATCCTACCCCTTATCATCATCAGCCCTCG	180
phac.afr	CAACTCTAACACGATTCTTGCCTTCCACTTCATTTACCTTTATCATCGCTGCCCTAG	180
sus.bar	CAACCCCTAACACGATTCTTGCCTTCCACTTTATCCTGCCATTATCATCATACGGCCCTCG	180
sus.scr.ewb3	CAACCCCTAACACGATTCTTGCCTTCCACTTTATCCTACCTTGTCAATTGCAGCTCTAG	180
lama.gla	CCACCCCTAACACGATTCTTGCCTTCCACTTTATCCTACCTTGTCAATTGCAGCTCTAG	180
lama.gua	CCACCCCTAACRCGATTCTTGCCTTCCACTTTATCCTACCTTGTCAATTGCAGCTCTAG	180
vic.vic	CCACCCCTAACCGATTCTTGCCTTCCACTTTATCCTACCTTGTCAATTGCAGCTCTAG	180
cam.bac	CCACCCCTAACACGATTCTTGCCTTCCACTTCATCCTGCCATTATCATACGGCCCTAG	180
arc.for	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTGCCATTATCATACGGCCCTAG	180
arc.gas	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTGCCATTATCATACGGCCCTAG	180
eum.jub	CAACCCCTAACACGATTCTTGCCTTCCACTTTATCCTGCCATTATCATACGGCCCTAG	180
zal.cal	CAACCCCTAACACGATTCTTGCCTTCCACTTTATCCTGCCATTATCATACGGCCCTAG	180
odo.zos	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTACCCATTGTAGTATCAGCACTAG	180
pho.fasciata	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTACCCATTGTAGTATCAGCACTAG	180
pho.gro	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTACCCATTGTAGTATCAGCACTAG	180
pho.vit	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTACCCATTGTAGTATCAGCACTAG	180
cys.cri	CAACTCTAACACGGTTTTTGCCCTTCCACTTCATCCTACCCATTGTAGTATCAGCACTAG	180
hyd.lep	CAACCCCTAACACGATTCTTGCCTTCCACTTTATCCTCCCTTGTAGTATCAGCACTAG	180
leg.wed	CAACCCCTAACACGATTCTTGCCTTCCACTTTATCCTCCCTTGTAGTATCAGCACTAG	180
mir.leo	CAACCCCTAACACGATTCTTGCCTTCCACTTTATCCTCCCTTGTAGTATCAGCACTAG	180
eri.bar	CAACCCCTAACACGATTCTTGCCTTCCACTTTATCCTCCCTTGTAGTATCAGCACTAG	180
mon.sch	CAACCCCTAACACGATTCTTGCCTTCCACTTTATCCTCCCTTGTAGTATCAGCACTAG	180
hela.mal	CAACCCCTAACACGATTCTTGCCTTCCACTTTATCCTCCCTTGTAGTATCAGCACTAG	180
sel.thi	CAACCCCTAACACGATTCTTGCCTTCCACTTTATCCTCCCTTGTAGTATCAGCACTAG	180
ail.ful	CAACCCCTAACACGATTCTTGCCTTCCACTTTATCCTCCCTTGTAGTATCAGCACTAG	180
fel	CAACCCCTAACACGATTCTTGCCTTCCACTTTATCCTCCCTTGTAGTATCAGCACTAG	180
can	CAACCCCTAACACGATTCTTGCCTTCCACTTTATCCTCCCTTGTAGTATCAGCACTAG	180
tal	CAACCCCTAACACGATTCTTGCCTTCCACTTTATCCTCCCTTGTAGTATCAGCACTAG	180
gla.sab	CAACCCCTAACACGATTCTTGCCTTCCACTTTATCCTCCCTTGTAGTATCAGCACTAG	180
gla.vol	CTACCCCTAACCGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
hyl.pha	CTACCCCTAACCGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
get.set	CTACCCCTAACCGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
bel.pea	CTACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
pte.mom	CTACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
gala.demi	CTACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
pero.pot	CTACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
gala.mat	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
gala.moh	CTACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
oto.gas	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
lor.tac	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
nyc.con	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
mus	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
gott	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
homo	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
dug.dug	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
ele.max	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
aff.son	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
pavo.mut	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
tsa.bly	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
tsa.gar	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
tsa.zeb	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
tsa.ten	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180
tsa.zeb	CAACCCCTAACACGATTCTTGCCTTCCACTTCATCCTCCCTTGTAGTATCAGCACTAG	180

cat.wal	CAACTCTCACCCGATTCTCACCCTGACTTCTCTTCCCTTGTAATTGCAGGAATCA	130
cro.cro	CAACCTCACCGATTCTTCGCCCTGACTTCTCTTCCCTTGTAATTGCAGGAATTA	130
sym.ree	CAACCTCACCGATTCTTCGCCCTGACTTCTCTTCCCTTGTAATTGCAGGAATCA	130
bam.cho	CAACTCTCACCGATTCTCACCCTGACTTCTCTTCCCTTGTAATTGCAGGAATTA	130
fra.fra	CAACCTCACCGATTCTCACCCTGACTTCTCTTCCCTTGTAATTGCAGGAATCA	130
ich.cru	CAACCTCACCGATTCTTCGCCCTGACTTCTCTTCCCTTGTAATTGCAGGAATTA	130
anc.par	CCACATTAACCTGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATGGCCCTCA	130
anc.vir	CCACATTAACCTGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATGGCCCTCA	130
gru.ant.ant	CCACATTAACCTGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTCA	130
gru.ant.gil	CCACATTAACCTGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTCA	130
gru.ant.sha	CCACATTAACCTGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTCA	130
gru.leu	CCACATTAACCTGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTCA	130
gru.can.pra	CCACATTAACCCGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTCA	130
gru.can.row	CCACATTAACCCGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTCA	130
gru.can.tab	CCACATTAACCCGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTCA	130
gru.can.can	CCACATTAACCCGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTCA	130
gru.ame	CCACATTAACCCGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTCA	130
gru.gru	CCACATTAACCCGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTCA	130
gru.mon	CCACATTAACCTGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTCA	130
gru.nig	CCACATTAACCTGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTCA	130
gru.jap	CCACATTAACCTGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTCA	130
cic.boy	CTACCTAACCCGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTTA	130
rhe.ame	CAACCTGACACGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTAG	130
ant.alb	CAACACTGACCCGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTCA	130
fal.fam	CAACACTAACCGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTCA	130
fal.ver	CAACACTGACCCGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTCA	130
fal.per	CAACACTAACCGTTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTTA	130
fal.spa	CAACCTAACCGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTCA	130
ayt.ame	CAACCTAACCGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTCA	130
smi.sha	CAACACTAACCGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTCA	130
vid.cha	CAACCTAACCGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTAA	130
chry.pic	CAACCTAACCGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTAA	130
emy.orb.kur	CAACCTAACCGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGCCTTA	130
che.mud	CAACCTCACCCGATTCTTCACCTTACACTTCTCTTCCATTCTAATTATAGGGCCCT	130
eum.egz	* * * * *	130
aep.mel	CCATAGTCCACCTACTCTTCTTCACGAAACAGGATCTAACACCCCTACAGGAATCTCAT	140
ore.ore	CCATAGTACACCTACTCTTCTTCACGAAACAGGATCTAACACCCCTACAGGAATCTCAT	140
add.nas	CCATAGTCCATCTACTCTTCTTCACGAAACAGGATCTAACACCCCTACAGGAATCTCAT	140
ory.dam	CCATAGTCCACCTACTCTTCTTCACGAAACAGGATCTAACACCCCTACAGGAATCTCAT	140
big.equ	CCATAGTACACCTACTCTTCTTCATGAGACAGGATCTAACACCCCTACAGGAATTTCAT	140
alc.bus	CCATAGTTCACCTTTTATTCTTCACGAAACAGGATCTAACACCCCTACAGGAATCTCAT	140
sig.lig	CCATAGTTCACCTTTTATTCTTCACGAAACAGGATCTAACACCCCTACAGGAATCTCAT	140
bea.hun	CCATAGTTCACCTTTTATTCTTCACGAAACAGGATCTAACACCCCTACAGGAATCTCAT	140
dam.lun	CCATAGTTCACCTTTTATTCTTCACGAAACAGGATCTAACACCCCTACAGGAATTTCAT	140
con.tau	CTATAGTCCATCTCTTATTCTTCACGAAACAGGATCTAACACCCCTACAGGAATTTCAT	140
amm.les	CCATAGTCCACCTRACTTTCTTCATGAGACAGGATCTAACACCCCTACAGGAATTTCAT	140
pse.nay	CCATAGTCCACCTTRACTTTCTTCACGAAACAGGATCTAACACCCCTACAGGAATCTCAT	140
cap.ibe	CCATAGTCCACCTTRACTTTCTTCACGAAACAGGATCTAACACCCCTACAGGAATCTCAT	140
hem.jem	CCATAGTCCACCTTRACTTTCTTCACGAAACAGGATCTAACACCCCTACAGGAATCTCAT	140
cap.fal	CCATAGTCCACCTTRACTTTCTTCACGAAACAGGATCTAACACCCCTACAGGAATCTCAT	140
sup.pyc	CCATAGTCCACCTTRACTTTCTTCACGAAACAGGATCTAACACCCCTACAGGAATCTCAT	140
sup.sup	CCATAGTCCACCTTRACTTTCTTCACGAAACAGGATCTAACACCCCTACAGGAATCTCAT	140
rem.tan	CTATAGTCCACCTTRACTTTCTTCACGAAACAGGATCTAACACCCCTACAGGAATTTCAT	140
bud.tan.BAN	CCATAGTCCACCTTATTTCTTCACGAAACAGGATCTAACACCCCTACAGGAATTTCAT	140
pan.hod	CCATAGTCCACCTTATTTCTTCACGAAACAGGATCTAACACCCCTACAGGAATTTCAT	140
ovi.amm	CCATAGTCCACCTTATTTCTTCACGAAACAGGATCTAACACCCCTACAGGAATTTCAT	140

ovi.vig	CTATAGTTCACCTACTTTCTCCACGAAACAGGATCCAATAACCCCACAGGAATTCCAT	240
cap.cri	CCATAGTGCACCTACTTTCTCCACGAAACAGGATCCAACACCCCACAGGAATTCCAT	240
ovi.mos	CTATAGTACATTGCTTTCTCCACGAAACAGGATCCAACACCCCACAGGAATTCCAT	240
ore.ame	CCATAGTCCACCTACTTTCTCCACGAAACAGGATCTAATAACCCCACAGGAATTCCAT	240
cep.dor	CCATAGTTCACCTACTTTCTCCATGAAACAGGATCCAACACCCCACAGGAATTCCAT	240
cep.max	CCATAGTCCACCTACTTTCTCCACGAAACAGGATCTAATAACCCCACAGGAATTCCAT	240
bis.ben	CCATAGTTCACCTACTTTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
bos.gru	CCATAGTCCACCTACTTTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
bos.tra	CAATAATCCATCTACTTTCTCCATGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
bub.min	CAATAGTCCACCTATTATTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
buba.bub	CAATAGTCCACCTATTATTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
tra.ang	TTATGGTCACCTATTATTCTCCATGAAACAGGATCCAACACCCCACAGGAATTCCAT	240
tra.eur	CCATGGTACACCTACTATTCTCCACGAAACAGGATCCAACACCCCACAGGRATCTCAT	240
kob.ell	CCATAGTCCATCTTCTGTTCTCCATGAAACAGGATCCAATAACCCCACAGGAATTCCAT	240
kob.meg	CTATAGTCCACCTACTATTCTCCACGAAACAGGATCCAACACCCCACAGGGATTTCAT	240
red.azu	CTATAGTCCACCTACTATTCTCCACGAAACAGGATCCAACACCCCACAGGGATTTCAT	240
red.ful	CTATAGTCCACCTACTTTCTCACGAAACAGGATCCAACACCCCACAGGAATTCCAT	240
neo.mos	CCATAGTCCACCTACTTTCTCACGAAACAGGATCTAACACCCCACGGGAATTCCAT	240
pel.cap	CCATAGTACACTTGCTTTCTCCATGAAACAGGATCCAACACCCCACAGGAATTCCAT	240
gaz.dam	CCATAGTTCTCTATTATTCTCCACGAAACAGGATCCAACACCCCACAGGAATTCCAT	240
our.our	CCACAGTCCACCTACTATTCTCCACGAAACAGGGATCCAACACCCCACAGGAATTCCAT	240
ant.cer	CCATAGTACACCTACTGTCTTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
sai.tat	CTATAGTCCACCTACTTTTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
mad.kir	CCATGGTCACCTCTTCTCCATGAAACGGGATCCAACACAGGGATTTTAT	240
rap.mei	CTATAGTCCACCTACTTTTCTCCACGAAACTGGATCTAACACCCCACAGGAATTCCAT	240
gaz.gaz	CTATAGTCCACCTATTATTCTCCATGAAACGGGATCTAACACCCCACAGGAATTCCAT	240
ant.ame	CCATAGTACACTTACTATTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
hyd.ina	CCATAGTGCACCTACTTTTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
mun.mun	CTATAGTCCACCTACTTTTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
alc.alc	CCATAGTCCACCTACTTTTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
cer.el.a.kan	CTATAGTACACTTACTCTTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
cer.el.a.xan	CTATAGTACACTTACTCTTCTCCACGAGACAGGATCTAACACCCCACAGGAATTCCAT	240
cer.el.a.can	CTATAGTACACTTACTCTTCTCCACGAGACAGGATCTAACACCCCACAGGAATTCCAT	240
cer.nip.cent	CTATAGTACACTTACTCTTCTCCACGAGACAGGATCTAACACCCCACAGGAATTCCAT	240
cer.nip.yes	CTATAGTACACTTACTCTTCTCCACGAGACAGGATCTAACACCCCACAGGAATTCCAT	240
cer.nip.ker	CTATAGTACACTTACTCTTCTCCACGAGACAGGATCTAACACCCCACAGGAATTCCAT	240
cer.nip.pul	CTATAGTACACTTACTCTTCTCCACGAGACAGGATCTAACACCCCACAGGAATTCCAT	240
cer.nip.nip	CTATAGTACACTTACTCTTCTCCACGAGACAGGATCTAACACCCCACAGGAATTCCAT	240
cer.el.a.sco	CTATAGTACACTTACTCTTCTCCACGAGACAGGATCTAACACCCCACAGGAATTCCAT	240
cer.dam	CTATAGTACACTTACTCTTCTCCACGAGACAGGATCTAACACCCCACAGGAATTCCAT	240
ran.tar	CTATAGTACACTTACTCTTCTCCACGAGACAGGATCTAACACCCCACAGGAATTCCAT	240
mos.fus	CTATAGTACACTTACTCTTCTCCACGAGACAGGATCTAACACCCCACAGGAATTCCAT	240
mos.leu	CTATAGTACACTTACTCTTCTCCACGAGACAGGATCTAACACCCCACAGGAATTCCAT	240
mos.chr	CTATAGTACACTTACTCTTCTCCACGAGACAGGATCTAACACCCCACAGGAATTCCAT	240
mos.bet	CTATAGTACACTTACTCTTCTCCACGAGACAGGATCTAACACCCCACAGGAATTCCAT	240
mos.mos	CCATGGTTCATCTACTTTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
tri.jay	TCCTAGTCCACCTTTTATTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
crig.cap	CCCTACTCCATCTTCTCCACGAGACAGGATCTAACACCCCACAGGAATTCCAT	240
bala.acu	CAATTGTCACCTCATTTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
bala.bon	CAATTGTCACCTCATTTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
bala.bet	CAATTGTCACCTCATTTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
bala.edi	CAATTGTCACCTCATTTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
esch.coo	CAATTGTCACCTCATTTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
bala.mus	CAATTGTCACCTCATTTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
megz.sow	CAATTGTCACCTCATTTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
bala.phy	CAATTGTCACCTCATTTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
clip.mic	CAATTGTCACCTCATTTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240
depb.com	CAATTGTCACCTCATTTCTCCACGAAACAGGATCTAACACCCCACAGGAATTCCAT	240

ceph.eut	CAGCCGTCCACCTACTATTCTACACGAAAACAGGGATCCAACAAACCCCACAGGAATCCCAT	240
lage.obl	CAGCCGTCCACCTACTATTCTACACGAAAACAGGGATCCAACAAACCCCACAGGAATCCCAT	240
ceph.hea	CAGCCGTCCACCTACTATTCTACACGAAAACAGGGATCCAACAAACCCCACAGGAATCCCAT	240
ceph.hec	CAGCCGTCCACCTACTATTCTACACGAAAACAGGGATCCAACAAACCCCACAGGAATCCCAT	240
lage.aus	CAGCCGTCCACCTACTATTCTACACGAAAACAGGGATCCAACAAACCCCACAGGAATCCCAT	240
lage.cru	CAGCCGTCCACCTGCTATTCTACACGAAAACAGGGATCCAACAAACCCCACAGGAATCCCAT	240
lage.obs	CAGCCGTCCACCTACTATTCTACACGAAAACAGGGATCCAACAAACCCCACAGGAATCCCAT	240
lisso.bor	CAGCTGTTCACCTACTATTCTACACGAAAACAGGGATCCAACAAACCCCACAGGAATCCCAT	240
lisso.per	CAGCTGTTCACCTACTGTTCCTACACGAGAACAGGGATCCAATAACCCCACAGGAATCCCAT	240
glo.mac	TAGCTGTCACCTGCTATTCTACACGAAAACAGGGATCCAATAACCCCACAGGAATCCCAT	240
glo.mel	TAGCTGTTCACCTGCTATTCTACACGAAAACAGGGATCCAATAACCCCACAGGAATCCCAT	240
fere.att	TAGCTGTCACCTGCTATTCTACACGAAAACAGGGATCCAATAACCCCACAGGAATCCCAT	240
pepo.ele	TAGCTGTCACCTGCTATTCTACACGAGAACAGGGATCCAATAACCCCACAGGAATCCCAT	240
gram.gri	CAGCTACCCACCTACTATTCTACACGAGACTGGATCCAATAACCCCACAGGAATCCCAT	240
pse.cra	CAGCTGTTCACCTGCTTCTACACGAGAACAGGGATCCAATAACCCCACAGGAATCCCAT	240
lage.acu	CAGCTGTTCACCTACTGTTCCTACACGAGAACAGGGATCCAATAACCCCACAGGAATCCCAT	240
orci.bre	TAACCTGTCACCTACTATTCTACACGAAAACAGGGATCCAACATAACCCCACAGGAATCCCAT	240
orca.bre	CAGCCGTTCACCTGCTATTCTACACGAAAACAGGGATCCAATAACCCCACAGGAATCCCAT	240
del.cap	CAGCCGTTCACCTGCTATTCTACACGAAAACAGGGATCCAATAACCCCACAGGAATCCCAT	240
del.tro	CAGCCGTTCACCTGCTATTCTACACGAAAACAGGGATCCAATAACCCCACAGGAATCCCAT	240
del.del	CAGCCGTTCACCTGCTATTCTACACGAAAACAGGGATCCAATAACCCCACAGGAATCCCAT	240
sten.cly	CAGCCGTTCACCTGCTATTCTACACGAAAACAGGGATCCAATAACCCCACAGGAATCCCAT	240
sten.coe	CAGCCGTTCACCTGCTATTCTACACGAAAACAGGGATCCAATAACCCCACAGGAATCCCAT	240
tur.adu	CAGCCGTTCACCTACTATTCTACACGAAAACAGGGATCCAATAACCCCACAGGAATCCCAT	240
sten.fro	CAGCCGTTCACCTACTATTCTACACGAAAACAGGGATCCAATAACCCCACAGGAATCCCAT	240
saus.chi	TAGCCGTTCACCTGCTATTCTACACGAAAACAGGGATCCAATAACCCCACAGGAATCCCAT	240
sten.lon	CAGCCGTTCACCTACTATTCTACACGAAAACAGGGATCCAACAACCCCACAGGAATCCCAT	240
turs.tru	CAGCCGTTCACCTACTATTCTACACGAAAACAGGGATCCAACAACCCCACAGGAATCCCAT	240
lage.alb	TAGCTGTCACCTACTATTCTACACGAGAACAGGGATCCAACATAACCCCACAGGAATCCCAT	240
sten.bre	CAACTGTCACCTACTATTCTACACGAGAACAGGGATCCAACATAACCCCACAGGAATCCCAT	240
sota.flu	CAGCCGTTCACCTACTATTCTACACGAAAACAGGGATCCAACAACCCCACAGGAATCCCAT	240
del.leu	TAGCCGTTCACCTACTATTCTACACGAAAACAGGGATCCAACATAACCCCACAGGAATCCCAT	240
mono.mon	TGGCCGTCACCTATTCTACACGAAAACAGGGATCCAACATAACCCCACAGGAATCCCAT	240
plat.gan	CAATTATCACCTACTATTCTACACGAAAACAGGGCTAAACAAACCCCACAGGAATCCCAT	240
plat.min	CAGTTATCACCTACTATTCTACACGAAAACAGGGCTAAACAAACCCCACAGGAATCCCAT	240
kogi.bre	CAATGGTCACCTCTTATTCTACACGAAAACAGGGATCCAACAAACCCCACAGGAATCCCAT	240
kogi.sim	CAATAATCACCTCTTATTCTACACGAAAACAGGGATCCAACAAACCCCACAGGAATCCCAT	240
phys.cat	CAATAGTACATCTCTTATTCTACACGAAAACAGGGCTAAACAAACCCCACAGGAATCCCAT	240
lipo.vex	CAACCGTCACCTACTATTCTACACGAAAACAGGGCTAAACAAACCCCACAGGAATCCCAT	240
phoc.sin	TAATCGTCATCTACTATTCTACACGAAAACAGGGCTAAACAAACCCCACAGGAATCCCAT	240
bera.bai	CAGCCGTCACCTACTATTCTACACGAAAACAGGGATCCAACAAACCCCACAGGAATCCCAT	240
ziph.car	CAGCCGTCACCTACTATTCTACACGAAAACAGGGATCTAAATAACCCCACAGGAATCCCAT	240
meso.eur	CAATCGTCACCTACTATTCTACACGAAAACAGGGATCTAAATAACCCCACAGGAATCCCAT	240
meso.bid	CAATCGTCACCTACTATTCTACACGAAAACAGGGATCTAAATAACCCCACAGGAATCCCAT	240
meso.den	CAATCGTCACCTACTATTCTACACGAAAACAGGGATCTAAATAACCCCACAGGAATCCCAT	240
hype.amp	CAATCGTCACCTACTATTCTACACGAAAACAGGGATCTAAATAACCCCACAGGAATCCCAT	240
meso.per	CAATTGTCATCTACTATTCTACACGAAAACAGGGATCTAAATAACCCCACAGGAATCCCAT	240
ponc.bla	TTATAGTCACCTGCTATTCTACACGAAAACAGGGATCTAAATAACCCCACAGGAATCCCAT	240
hex.lib	CCGGCCGTCACCTACTATTCTACACGAAAACAGGGATCTAAATAACCCCACAGGAATCCCAT	240
hipp.amp	CCATCGTCATCTACTATTCTACACGAAAACAGGGATCTAAACAACCCCACAGGAATCCCAT	240
dic.sum	CAATTACCCACCTGCTATTCTACACGAAAACAGGGATCTAAACAACCCCACAGGAATCCCAT	240
chin.son	CGATCACCCACCTACTATTCTACACGAAAACAGGGATCTAAACAACCCCACAGGAATCCCAT	240
cera	CAATCACCCACCTACTATTCTACACGAAAACAGGGATCTAAACAACCCCACAGGAATCCCAT	240
equu	TAATCGTCATCTACTATTCTACACGAAAACAGGGATCTAAACAACCCCACAGGAATCCCAT	240
baby.bab	CAACCGTCACATCTTCTTCTACACGAAAACAGGGATCTAAACAACCCCACAGGAATCCCAT	240
phac.afr	CAACCGTCACATCTTCTTCTACACGAAAACAGGGATCTAAACAACCCCACAGGAATCCCAT	240
sus.bac	CAGCCSTACATCTTCTTCTACACGAAAACAGGGATCTAAACAACCCCACAGGAATCCCAT	240
slug.scc.swb1	CAGCCSTACATCTTCTTCTACACGAAAACAGGGATCTAAACAACCCCACAGGAATCCCAT	240

lama.gla	CAGGAGTACATCTACTATTTTACACGAAACAGGCTCCAACAACTCCAAACAGGAATTCTT	240
lama.gua	CAGGAGTGCATCTACTATTTTACACGAAACAGGCTCCAACAACTCCAAACAGGAATTCTT	240
vic.vic	CGGGAGTACATCTACTATTTTACACGAAACAGGCTCCAACAACTCCAAACAGGAATTCTT	240
cam.bac	TAGCCGTACACCTATTCTACACGAAACAGGCTTAATAACCCGACAGGAATCTCT	240
arc.for	TAATAGTACATCTGTATTCTACATGAAACAGGATCCAATAACCCATCAAGAGTCTCT	240
arc.gaz	TAATAGTGCACCTACTATTCTACACGAAACAGGATCCAACAAACCCATCAAGAGTCTCT	240
eum.jub	TAATAGTACACCTATTCTACACGAAACTGGATCCAACAACTCCATCAAGGAATCTCT	240
zal.cal	TAATAGTACACCTATTCTACACGAAACTGGATCCAACAAACCCATCAAGGAATCTCT	240
odo.ros	CAGCAGTACACCTACTATTCTACACGAAACAGGATCCAACAAACCCCTCCGGAAATCGTAT	240
pho.fasciata	CGCCAGITCACCTACTATTCTACACGAAACAGGATCCAACAAACCCACCGGAATCGTAT	240
pho.gro	CGGCAGTTCATCTACTATTCTACACGAAACAGGATCAAACAAACCCCTCCGGAAATCATAT	240
pho.vit	CAGCAGTCACCTACTATTCTACACGAAACAGGATCTAATAACCCCTCCGGAAATCACAT	240
cys.cri	CAACAGTCACCTACTATTCTACACGAAACAGGATCTAATAACCCCTCCGGAAATTCCAT	240
hyd.lep	CAGCAGTACATCTACTATTCTACACGAAACAGGATCCAACAAACCCCTCCGGAAATTCCAT	240
lep.wed	CAGCAGTACATCTACTATTCTACACGAGACAGGATCCAACAAACCCCTCTGGAAATCCCAT	240
mir.leo	CAGCAGTACATCTACTATTCTACACGAAACAGGATCCAACAAACCCCTCTGGAAATCTCGT	240
eri.bar	CAGCAGTCACCTATTCTACACGAAACAGGATCCAACAAACCCCTCTGGAAATTCGT	240
mon.sch	CAGCAGTCATTTATTCTACACGAAACAGGATCCAACAAACCCCTCTGGAAATCCCAT	240
hela.mal	CAGCGGTCCACCTATTCTACACGAAACAGGCTCCAACAAACCCCTCTGGAAATCCCAT	240
sel.thi	CAGCAGTTCATCTATTGTCCTACACGAAACAGGATCCAACAAACCCCTCTGGAAATCCCAT	240
ail.ful	CAACTATCCATCTCTATTCTACATGAAACAGGATCTAATAACCCCTCAGGCATCCAT	240
fel.	CAGGAGTACACCTCTATTCTCATGAAACAGGATCTAACAACCCCTCAGGAATTACAT	240
can	CAATAGTACACCTCCTATTCTACACGAAACCGGATCCAACAAACCCCTCAGGAATCACAT	240
tal	CTGGAGTTACCTGTATTCTCACGAAACAGGATCAAACAAACCCATCAGGACTCTCAT	240
gla.sab	CCATAATTCCATCTACTCTTCTACACGAAACAGGATCAAACAAACCCATCAGGACTCTCAT	240
gla.vol	CTATAATTCCACCTCTCTTCTACACGAAACAGGATCAAACAAACCCATCAGGCTCTATT	240
byl.pha	CTATAATTCCACCTCTCTTCTACACGAAACAGGCTCAAATAATCCATCAGGTCTATT	240
pet.set	CAATAGTCACCTCTTCTCCACGAAATTGGGCTAAATAACCCCCGGATTATT	240
bel.pea	CAATAGTTCACCTACTTTCTCATGAAACAGGCTCAAACAAACCCATCTGGACTTACCT	240
pte.mom	TCATAATTCCACCTCTTCTACACGAAACAGGATCAAACAAACCCCTCAGGACTCTCAT	240
gala.demi	CCACAACTCACCTCTTCTACACGAAACAGGCTCAAATAACCCRGCGAGGAATTCCAT	240
pero.poc	CCATAATTCCACCTCTTCTACATGAAACAGGATCAAACAAACCCCTCAGGAATCTCAT	240
gala.mat	CCATAATTCCACCTCTTCTACATGAAACAGGCTCAAATAACCCCTCAGGAATCTCAT	240
gala.moh	CCATAATTCCACCTCTTCTACATGAAACAGGCTCAAATAACCCCTCAGGAATCTCAT	240
oto.gar	TCATAATTCCACCTCTTCTACATGAAACAGGCTCAAATAACCCCTCAGGAATCTCAT	240
lor.tar	CTGGCAATTTCACCTACTTTCTACAGGATCAAACAAACCCATCAGGACTCTCAT	240
nyc.cou	TTGTGATTTCACCTCATCTTCTACATGAAACAGGCTCAAATAACCCATCAGGACTCTCAT	240
mus	CAATCGTTACCTCTTCTCCACGAAACAGGATCAAACAAACCCCTCAGGATTAACAT	240
gorr	CAACCCCTCCATCTCTATTCTACACGAAACAGGATCAAACAAACCCCTCAGGATCCCT	240
homo	CAACACTCCACCTCTTCTACACGAAACAGGATCAAACAAACCCCTCAGGAATCACCT	240
dug.dug	TAATAGTCACCTACTATTCTCCACGAAACAGGCTCAAACAAACCCACGGGACTGATGT	240
ele.max	CAGGAGTGCACCTAACCTTCTACACGAAACAGGCTCAAACAAACCCACTAGGCTCTCAT	240
air.con	CAATTATCCACCTCACATTCTCATGAAATCAGGCTCAAACAAACCCACTGGGATCTCAT	240
pavo.mut	CAATTATCCACCTCACATTCTCATGAAATCAGGCTCAAATAATCCACTAGGATCTCAT	240
tra.bly	CCATCATGCACCTCATCTTCTACATGAAATCAGGCTCAAATAACCCACTGGGATCTCAT	240
tra.sac	CTATCATACACCTCATCTTCTACATGAAATCAGGCTCAAACAAACCCCTGGGATCTCAT	240
tra.cob	CCATCATCCACCTCATCTTCTACATGAAATCAGGCTCAAACAAACCCCTGGGATCTCAT	240
tra.zem	CCATCATCCACCTCACATTCTACACGAAATCAGGCTCAAACAAACCCACTGGGATCTCAT	240
arg.arg	CCATCACCCATCTCATATTCTACATGAAATCAGGCTCAAATAACCCCTGGGATCTCAT	240
cat.wal	CTGTCAACCCACCTCATATTCTACACGAAATCAGGCTCAAACAAACCCACTAGGATCTCAT	240
cro.cro	CCATCACACATCTTCTACACGAAATCAGGCTCAAACAAACCCACTAGGATCTCAT	240
sym.ree	CCATTATCCACCTCACATTCTACACGAAATCAGGCTCAAACAAACCCCTAGGATCTCAT	240
bam.sho	CTATCATCCACCTCACATTCTACACGAAATCAGGCTCAAACAAACCCACTAGGATCTCAT	240
sea.fra	CTGTCAACCCACCTCATATTCTACACGAAATCAGGCTCAAACAAACCCACTAGGATCTCAT	240
ith.cri	CCCTAATCCACCTCACATTCTACACGAAATCAGGCTCAAACAAACCCACTAGGATCTCAT	240
int.pac	CCCTAATCCACCTCACATTCTACACGAAATCAGGCTCAAACAAACCCACTAGGATCTCAT	240
int.vic	CCCTAATCCACCTCACATTCTACACGAAATCAGGCTCAAACAAACCCACTAGGATCTCAT	240
gca.mrc	CCCTAATCCACCTCACATTCTACACGAAATCAGGCTCAAACAAACCCACTAGGATCTCAT	240

gru.ant.gil	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCCTAGGCATCGTAT	240
gru.ant.sha	CCCTAATCCACCTCACCTTCTTACGAATCCGGTTCAAACAACCCCCCTAGGCATCGTAT	240
gru.leu	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCCTAGGCATCGTAT	240
gru.can.pra	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCCTAGGCATCGTAT	240
gru.can.row	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCCTAGGCATCGTAT	240
gru.can.tab	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCCTAGGCATCGTAT	240
gru.can.can	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCCTAGGCATCGTAT	240
gru.ame	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCCTAGGCATCGTAT	240
gru.gru	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCCTAGGCATCGTAT	240
gru.mon	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCCTAGGCATCGTAT	240
gru.nig	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCCTAGGCATCGTAT	240
gru.jap	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCCTAGGCATCGTAT	240
cic.boy	CCCTAATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCCTAGGCATCGTAT	240
rhe.ame	CTCTTATCCACCTCACCTTCTTACGAATCCGGCTCAAACAACCCCCCTAGGAATCGTAT	240
ant.alb	TCTTAATTCACTGGCATTCTCCACGAATCAGGCTCAAACAACCCACTAGGCATCACAT	240
fal.fam	CCTTAATTCCACCTCACCTTCTTACATGAATCAGGTTCAAACAACCCCCCTAGGAATTCACAT	240
fal.ver	CCCTTAATTCACTTCACCTTCTTACCGAATCAGGTTCAAACAACCCCCCTAGGAATTCACAT	240
fal.per	CCCTTAATTCACTTCACCTTCTTACATGAATCAGGCTCAAATAACCCCCCTAGGAATTCACAT	240
fal.spa	CCCTTAATTCCACCTCACCTTCTTACATGAATCAGGTTCAAACAACCCCCCTAGGAGTCACAT	240
ayt.ame	CCCTAGTCCACCTAACCTTCTTACCGAGTCAGGCTCAAACAACCCCCCTAGGCATTGTAT	240
smi.sha	CACTCATCCATCTCACCTTCTTACATGAAACAGGTTCAAACAACCCCTCTAGGTATCTCAT	240
vid.cha	CTCTAGTCCACCTCACATTCTTACCGAAACAGGATCAAACAATCCAATAGGAATTCCAT	240
chry.pic	CAATAGTACACCTACTTTTCTACATGAAACTGGATCAAACAACCCAAACAGGGATTAACCT	240
emy.orb.kur	CAATAGTACACCTACTCTTCTACCGAAACAGGATCAAACAACCCAAACAGGGATTAACCT	240
che.mud	CGCGAGTACATCTATTATTCCTGCACGAAACAGGATCAAACAACCCAAACAGGGATTAACCT	240
eum.egr	CAATAATTCACTACTATTCTTACCGAAACAGGATCAAACAACCCAAACAGGGACTAAACCT	240

\* \* \* \* \*

aep.mel	CAGATTCAAGATAAAAATTCCATTCCACCCCTTACTATACTATTRAAGACATCCTAGGAATCC	300
ore.ore	CGACACAGACAAAATTCCATTCCATCCCTTATTACACATCAAAGATATCCTAGGGGCC	300
add.nas	CGACACAGACAAAATTCCATTCCACCCCTTACTATACTACATCAAAGATATCCTAGGGGCC	300
ory.dam	CGACACAGACAAAATTCCGTTCCACCCCTTATTACACATCAAAGATATCCTAGGGGCC	300
hip.equ	CGACTCCGATAAAAACCCCATTCCACCCCTACTACACCATCAAAGACATTCTAGGGGCC	300
alc.bus	CGACCCGAGATAAAAATTCCATTCCACCCCTACTACACATCAAAGGACATTCTAGGGGCC	300
sig.lic	CGACCGAGATAAAAATTCCATTCCACCCCTACTACACATCAAAGGACATTCTAGGGGCC	300
bea.hun	CGATGCAGATAAAAATTCCATTCCACCCCTACTACACCATCAAAGACATTCTAGGGGCC	300
dam.lun	CGATGCCGAGACAAAATTCCGTTCCACCCCTACTACACTACATCAAAGACGCCCTAGGGGCC	300
con.cau	CCGACACCGATAAAAATTCCATTCCACCCCTTACTACACCATCAAAGACATTCTAGGGGCC	300
amm.ler	CAGACGAGACAAAATTCCATTCCACCCCTTACTACACCATCAAAGATATTCTAGGGGCC	300
pse.nay	CAGACACAGACAAAATTCCATTCCACCCCTTACTACACCATCAAAGATATTCTAGGGGCC	300
cap.ibe	CAGACACAGACAAAATTCCATTCCACCCCTTACTACACCATCAAAGATATTCTAGGGGCC	300
hem.jem	CAGATACAGACAAAATTCCATTCCACCCCTTACTACACCATCAAAGATATTCTAGGGGCC	300
cap.fal	CAGACACAGACAAAATTCCATTCCACCCCTTACTACACCATCAAAGATATTCTAGGGGCC	300
rup.pyr	CAGATGCCGATRAAAATTCCATTCCACCCCTTACTACACCATCAAAGACATTCTGGGGCCA	300
rup.rup	CAGATGCCGACACAAAATTCCATTCCACCCCTTACTACACCATCAAAGACATTCTGGGGCCA	300
nem.cau	CAGACATAGACACAAAATTCCATTCCACCCCTTACTACACCATCAAAGATATTCTAGGGGCC	300
bud.tax.tax	CAGATGCAGATAAAAATTCCATTCCACCCCTTACTACACCATCAAAGATATTCTAGGGGCC	300
pan.hod	CAGATGCAGACAAAATTCCATTCCACCCCTTACTACACCATCAAAGACATTCTGGGGCCA	300
ovi.amm	CGAACACAGATAAAAATTCCATTCCACCCCTTACTACACCATCAAAGACATTCTGGGTGCC	300
ovi.vig	CGAACACAGACAAAATTCCATTCCACCCCTTACTACACCATCAAAGATATTCTAGGGGCC	300
cap.cri	CACACACACACAAAATTCCATTCCACCCCTTACTACACCATCAAAGACATTCTAGGGGCC	300
ovi.mos	CACACACGGACACAAAATTCCATTCCACCCCTTACTACACCATCAAAGACATTCTAGGGGCC	300
ore.ame	CACACACGACACAAAATTCCATTCCACCCCTTACTACACCATCAAAGACATTCTAGGGGCC	300
cep.dor	CGAACCGAGACACAAAATTCCATTCCACCCCTTACTACACCATCAAAGACATTCTAGGGGCC	300
cep.max	CACACCGAGACACAAAATTCCATTCCACCCCTTACTACACCATCAAAGACATTCTAGGGGCC	300
bis.bon	CACACCCGAGACACAAAATTCCATTCCACCCCTTACTACACCATCAAAGACATTCTAGGGGCC	300
bos.gru	CACACCCGAGACACAAAATTCCATTCCACCCCTTACTACACCATCAAAGACATTCTAGGGGCC	300
bot.bca	CACACCCGAGACACAAAATTCCATTCCACCCCTTACTACACCATCAAAGACATTCTAGGGGCC	300

bub.min	CAGACACACACAAAATCCCATTCCACCCCTACTACACCATTAAACACATTCTAGGGCCCC	300
buba.bub	CAGACACAGACAAAATCCCATTCCACCCCTATTACACCATTAAAGACATCCTAGGGCCCC	300
tra.ang	CAGACATAGACAAAATCCCATTCCACCCCTATTACACTATCAAGGACATCCTAGGGCCCC	300
tra.eur	CRAACATAGACAAAATCCCATTCCACCCCTACTACACTATTAAAGGACATCCTAGGTGCC	300
kob.ell	CAGACATAGATAAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGGCCCC	300
kob.meg	CAGACACAGACAAAATCCCATTCCACCCATATTATACCATORAAAGATAATTCTAGGTGCC	300
zed.aru	CAGATGTAGACAAAATCCCATTCCATCTACTATRACTATCAAGGACCTCTAGGGCCCC	300
zed.ful	CAGAYATGGACAAAATCCCATTCCACCCNTACTRACTACACCATTAAAGACATTCTAGGGCCCC	300
neo.mos	CAGACGCAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGGCCCC	300
pel.cap	CCGACATAGACAAAATCCCATTCCACCCATACTACACCATTAAAGACATTCTAGGAGCAC	300
gaz.dam	CAGATCGAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGGGCC	300
our.our	CAGATGCAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGGGCC	300
ant.cer	CAGACGGAGACAAAATCCCATTCCACCCCTACTACACTATCAAGACATTCTAGGGGCC	300
sai.tat	CAGATTAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGGGCC	300
mad.kir	CAGACGGAGACGGAAATCCCATTCCACCCCTACTACACTATTAAAGACATTCTAGGGGCC	300
rap.mel	CAGATATAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGGGCC	300
gaz.gaz	CAGACGCAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGAGCAC	300
ant.ame	CAGACGCAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGAGCAC	300
hyd.ina	CAGATGCAGATAAATCCCATTCCATCTACTACACCATTAAAGACATTCTAGGTGTAC	300
mun.mun	CAGATGTAGACAAAATCCCATTCCATCTACTACACCATTAAAGACATTCTAGGTGCC	300
alc.alc	CAGACGCAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
cer.el.a.kan	CAGACGCAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
cer.el.a.xan	CAGACGCAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
cer.el.a.can	CAGACGCAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
cer.nip.cant	CAGACGCAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
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cer.nip.ker	CAGACGCAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
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cer.nip.nip	CAGACGCAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
cer.el.a.sco	CAGATGTAGATAAATCCCATTCCATCTACTACACCATTAAAGACATTCTAGGTGCC	300
cer.dam	CAGACTCAGATAAATCCCATTCCATCTACTACACCATTAAAGACATTCTAGGTGCC	300
tan.car	CAGATATAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
mos.fus	CAGATATAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
mos.leu	CAGATATAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
mos.chr	CAGACATAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
mos.ber	CAGACATAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
mos.mos	CAGACATAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
tra.jav	CAGACGCAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
trag.nap	CAGACGCAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
bala.acu	CTGACATAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
bala.bon	CTGATATAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
bala.bor	CCGACATAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
bala.edi	CCAACATAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
esch.rob	CCAACATAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
bala.mus	CTGACATAGATAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
mega.nov	CCAACATAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
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cap.mar	CCAACATAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGTGCC	300
ceph.com	CCAACATAGACATAATCCCATTCCACCCCTATTACACATTAAAGACATTCTAGGTGCC	300
ceph.eut	CCAACATAGACATAATCCCATTCCACCCCTATTACACATTAAAGACATTCTAGGTGCC	300
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ceph.hea	CCAACATAGACATAATCCCATTCCACCCCTATTACACATTAAAGACATTCTAGGTGCC	300
ceph.hed	CCAACATAGACATAATCCCATTCCACCCCTATTACACATTAAAGACATTCTAGGTGCC	300
lage.aus	CCAACATAGACATAATCCCATTCCACCCCTATTACACATTAAAGACATTCTAGGTGCC	300
lage.sru	CCAACATAGACATAATCCCATTCCACCCCTATTACACATTAAAGACATTCTAGGTGCC	300
lage.sbs	CCAACATAGACATAATCCCATTCCACCCCTATTACACATTAAAGACATTCTAGGTGCC	300
lissoc.bor	CCAACATAGACATAATCCCATTCCACCCCTATTACACATTAAAGACATTCTAGGTGCC	300
lissoc.psc	CCAACATAGACATAATCCCATTCCACCCCTATTACACATTAAAGACATTCTAGGTGCC	300

glo.mac	CCAAACATAGACATAATTCCATTCCACCCCTATTATAACAATTAAAGACATCCTAGGGGCC 300
glo.mel	CCAAACATAGACATAATTCCATTCCACCCCTATTATAACAATTAAAGATATCCTAGGGGCC 300
fere.att	CCAAACATAGACATAATTCCATTCCACCCCTATTATAACAATTAAAGATATCCTAGGTGCC 300
pepo.ele	CCAAACATAGACATAATTCCATTCCACCCCTATTATAACAATTAAAGACATCCTAGGGCTC 300
gram.gri	CCAAACATAGACATAATTCCATTCCACCCCTATTATAACAATTAAAGACATCCTAGGGGCC 300
pse.cra	CCAAACATAGACATAATTCCATTCCACCCCTATTATAACAATTAAAGACATCCTAGGGGCC 300
lage.acu	CTAACATAGATATAATTCCATTCCACCCCTATTATAACAATTAAAGATATCCTAGGGCTT 300
orci.bre	CCAAACATAGACATAATTCCATTCCACCCCTATTATAACAATTAAAGATATCCTAGGGGCC 300
orca.bre	CCAAACATAGACATAATTCCATTCCACCCCTATTATAACAATTAAAGACATCCTAGGTGCC 300
del.cap	CCAATATAGACATAATTCCATTCCACCCCTATTATAACAATTCAAGATATCCTAGGTGCC 300
del.tro	CCAATATAGACATAATTCCATTCCACCCCTATTATAACAATTCAAGATATCCTAGGTGCC 300
del.del	CCAATATAGACATAATTCCATTCCACCCCTATTATAACAATTCAAGATATCCTAGGTGCC 300
sten.cly	CCAATATAGACATAATTCCATTCCACCCCTATTATAACAATTAAAGATATCCTAGGTGCC 300
sten.coe	CCAATATAGACATAATTCCATTCCACCCCTATTATAACAATTAAAGACATCCTAGGTGCC 300
tur.adu	CCAATATAGACATAATTCCATTCCACCCCTATTATAACAATTCAAGACATCCTAGGTGCC 300
sten.fro	CCAATATAGACATAATTCCATTCCACCCCTATTATAACAATTCAAGACATCCTAGGTGCC 300
saus.chi	CCAATATAGACATAATTCCATTCCACCCCTATTATAACAATTCAAGACATCCTAGGTGGCT 300
sten.lon	CCAACATAGACATAATTCCATTCCACCCCTATTATAACAATTCAAGACATCCTAGGTGCC 300
turs.tru	CCAATATAGACATAATTCCATTCCACCCCTATTATAACAATTCAAGACATCCTAGGTGCC 300
lage.alb	CCAACATAGACATAATTCCATTCCACCCCTATTATAACAATTCAAGACATCCTAGGTGCC 300
sten.bre	CCAACATAGACATAATTCCATTCCACCCCTATTATAACAATTCAAGACATCCTAGGTGCC 300
sota.flu	CCAACATAGACATAATTCCATTCCACCCCTATTACACATCAAGACATCCTAGGTGCC 300
del.leu	CCAACATGGATAACAATTCCATTCCACCCCTACTACACAAATCAAGACATCCTAGGTGCC 300
mono.mon	CCAACATAGACATAATTCCATTCCACCCCTACTACACAAATCAAGACATCCTAGGGGCC 300
plat.gan	CCGACACTGACAAAATTCCATTCCACCCCTACTACACAAATCAAGACACCCCTAGGGGCC 300
plat.min	CCGACACTGACAAAATTCCATTCCACCCCTACTACACAAATCAAGACATCCTAGGGGCC 300
kogi.bre	CTGATATAGACAAAATTCCATTCCACCCCTACTACACAAATCAAGATATCCTAGGTGCC 300
kogi.sim	CCGACATAGACAAAATTCCATTCCACCCCTACTACACAAATCAAGACACCCATAGGTGCC 300
phys.cat	CTGACATAGACAAAATTCCATTCCACCCCTACTACACAAATCAAGACACTCTAGGGGCC 300
lipo.vex	CTAACATAGACAAAATTCCATTCCACCCCTACTACACAAATCAAGATATCCTAGGGGCC 300
phoc.sin	CTAACATAGACATAATTCCATTCCACCCCTACTACACAAATCAAGATATCCTAGGAGGCC 300
bara.bai	CCAATATAGATAAAAATTCCATTCCACCCCTACTACACAAATCAAGATATCCTAGGAGGCC 300
ziph.car	CCGATATAGACAAAATTCCATTCCACCCCTATTACACAAATCAAGACATCCTAGGGGCC 300
meso.eur	CTGATATAGACAAAATTCCATTCCACCCCTACTACACAAATCAAGATATCCTGGGAGGCC 300
meso.bid	CCGACATAGATAAAAATTCCATTCCACCCCTACTACACAAATTAAAGATATCCTGGGAGGCC 300
meso.dan	CTGACATAGATAAAAATTCCATTCCACCCCTATTACACAAATCAAGATATTTAGGAGGCC 300
hype.amp	CTGACATAGACAAAATTCCATTCCACCCCTACTACACAAATCAAGACACTCTAGGGGCC 300
meso.per	CTGACATAGACAAAATTCCATTCCACCCCTACTACACAAATCAAGATATTTAGGAGGCC 300
pont.bla	CTAACATAGATGCCATTCCATTCCACCCCTACTACACAAATTAAAGATATCCTGGGCGTAC 300
hex.lib	CAAACGCGAGACAAAATTCCATTCCACCCCTATTACACAAATCAAGGACATCCTAGGTATCC 300
hipp.amp	CAAACGCGAGACAAAATTCCATTCCACCCCTATTACACAAATCAAGGACATCCTAGGAGGCC 300
dic.sum	CTAACATAGACAAAATTCCATTCCACCCCTACTACACAAATCAAGAGATATCCTAGGAGGCC 300
shin.son	CTAACACAGACAAAATTCCATTCCACCCCTACTACACAAATCAAGAGACATCCTGGGAATTTC 300
cera	CCAACATAGACAAAATTCCATTCCACCCCTACTACACAAATTAAAGACATCCTAGGACTTC 300
equu	CTGACATAGACAAAATTCCATTCCACCCCTACTACACAAATTAAAGACATCCTAGGAGGCC 300
baby.bab	CAGATATAGACAAAATTCCATTCCACCCCTACTACACAAATTAAAGATATCCTAGGAGGCC 300
phac.afr	CAGACATAGACAAAATTCCATTCCACCCCTACTACACAAATTAAAGATATCCTAGGAGGCC 300
sus.bat	CAGACATAGACAAAATTCCATTCCACCCCTACTACACAAATTAAAGACATCCTAGGAGGCC 300
sus.sct.ewb3	CAGACATAGACAAAATTCCATTCCACCCCTACTACACAAATTAAAGACATCCTAGGAGGCC 300
lama.gla	CGGATATAGACAAAATTCCATTCCACCCCTACTACACAAATTAAAGACATCCTAGGAGTAC 300
lama.gua	CGGATATAGACAAAATTCCATTCCACCCCTACTACACAAATTAAAGACATCCTAGGAGGCC 300
vic.vic	GAGATATAGACAAAATTCCATTCCACCCCTACTACACAAATTAAAGACATCCTAGGAGGCC 300
cim.bac	CAGACATAGACAAAATTCCATTCCACCCCTACTACACAAATTAAAGACATCCTGGGAGGCC 300
acc.fec	CTGACTCGACACAAAATTCCATTCCACCCCTACTACACAAATTAAAGATATCCTGGGAGGCC 300
acc.gaz	CTGACTCGACACAAAATTCCATTCCACCCCTACTACACAAATTAAAGATATCCTGGGAGGCC 300
eum.jub	CCAACTCGACACAAAATTCCATTCCACCCCTACTACACAAATTAAAGACATCCTAGGAACTC 300
cal.cal	CTGACTCGACACAAAATTCCATTCCACCCCTACTACACAAATTAAAGACATCCTAGGAACTC 300
edr.zzz	CTGACTCGACACAAAATTCCATTCCACCCCTACTACACAAATTAAAGATATCCTAGGAGGCC 300

pho.fasciata	CCGACTCAGACAAAATCCCATTCCACCCATACTATAACAATTAAAGATATCCTAGGAGCCC	300
pho.gro	CCGACTCAGACAAAATCCCATTCCACCCATACTATAACAATTAAAGATATCCTAGGAGCCC	300
pho.vic	CCAACTCAGACAAAATCCCATTCCACCCATACTATAACAATTAAAGATATCCTAGGGCCC	300
cys.cri	CCGACTCAGACAAAATCCCATTCCACCCATACTATAACAATTAAAGACATCCTAGGAGCCC	300
hyd.lep	CCAACTCAGACAAAATCCCATTCCACCCATACTACACAATTCAAGACATCCTAGGAGCCC	300
leg.wed	CTGACTCAGACAAAATCCCATTCCACCCATACTACACAATTCAAGACATCCTAGGAGCCC	300
mir.leo	CCGACTCAGACAAAATCCCATTCCACCCATACTACAGTCAGGACATCCTAGGAGCT	300
eri.bar	CCAACTCAGACAAAATCCCATTCCACCCATACTATAACAATTAAAGACATTCTAGGAGCT	300
mon.sch	CCAACTCAGACAAAATCCCATTCCACCCATACTATAACAATTAAAGACATCCTAGGCGCC	300
hela.mal	CTGACTCAGACAAAATCCCATTCCACCCATACTACACAATTCAAGGACATCCTAGGCGCC	300
sel.thi	CCAACTCGGACAAAATCCCATTCCACCCATACTATAACAATTAAAGACGCCCTAGGCGCC	300
ail.ful	CCAACTCAGACAAAATCCCATTCCATTCCATTATAACAATTAAAGATATCTGGCGCTC	300
fel	CCGATTCAAGACAAAATCCCATTCCACCCATACTATAACAATTCAAGACATCCTAGGTCTC	300
can	CAGACTCAGACAAAATCCCATTCCACCCATACTACACAATTCAAGGATATCCTAGGAGCT	300
tal	CAGATACGGATAAAAATCCCATTCCACCCATTACACTATAAGACATCCTAGGAGCAC	300
gla.sab	CTGACTCAGATAAAAATCCCATTCCACCCATTCTCAATTAAAGACACCCCTAGGATTCT	300
gla.vol	CTGACTCAGACAAAATCCCATTCCACCCACTTCTCAATTAAAGATACCCCTAGGATTCT	300
hyl.pha	CCGATTCAAGACAAAATCCCATTCCACCCATACTATTCAATTAAAGATCTCCTAGGGCCC	300
pet.set	CCGATTCAAGACAAAATCCCATTCCACCCATACTATTCAATTAAAGATCTCCTAGGGCCC	300
bel.pea	CTGAATCTGATAAAAAGTACCAATTCCACCCATACTTCACATTAAAGATATTCTGGCGCC	300
pte.mom	CCGAATCCGACAAAATCCCATTCCACCCCTACTTCACATTAAAGACATTTAGGAGCAC	300
gala.demi	CAGACTCAGACAAAATCCCATTCCACCCCTATTACATAATTCAAGGATCTCCTAGGACTGA	300
pero.pot	CAGAATCAGACAAAATCCCATTCCACCCCTACTACACACACCAAGACTTAAGGAGCCA	300
gala.mat	CAGACTCCGACAAAATCCCATTCCACCCCTACTACACAATTAAAGACCTACTAGGAGTAA	300
gala.moh	CAGACTCCGACAAAATCCCATTCCACCCCTACTACACAATTAAAGACCTACTAGGAGCAA	300
oto.gar	CAGACTCTGACAAAATCCCATTCCACCCCTATTACACAATTAAAGACCTCTAGGAGCTA	300
lor.tar	CAGACTCTGACAAAATCCCATTCCACCCCTACTACACAATTAAAGATATTCTAGGAGTAA	300
nyc.cou	CAGACTCAGATAAGATCCATTCCACCCCTACTACTCACTAAAGACCTCTAGGAGTGG	300
mus	CAGATGAGATAAAAATCCCATTCCACCCCTACTACACAATTCAAGGATATCCTAGGTAATCC	300
gorr	CCCACTCTGACAAAATCCCATTCCACCCCTACTACACAATTCAAGGACATCCTAGGCCTAT	300
homo	CCCACTCCGATAAAAATCCCATTCCACCCCTACTACACAATTCAAGGACGCCCTGGCTTAC	300
dug.dug	CCGACTCAGACAAAATCCCATTCCACCCATAATTATTCACTCAAGGACCTCTAGGCCTAT	300
ele.max	CAGACTCAGACAAAATCCCATTCCACCCCTACTACACAATTCAAGGACTTCCTAGGCCTAT	300
afr.con	CCAATTCAAGATAAAAATCCCATTCCACCCGTACTACTCCCTCAAGGATATCCTAGGCTTAG	300
pavo.mut	CCAACTCAGACAAAATCCCATTCCACCCATACTACTCCCTCAAGGATATCCTAGGCTTAA	300
tra.bly	CTAACTCTGACAAAATCCCATTCCACCCGTACTACTCCCTCAAGGATATCCTGGGTCTAA	300
tra.sat	CCAACTCTGACAAAATCCCATTCCACCCATACTACTCCCTCAAGGATATCCTAGGCCTAA	300
tra.cob	CTGACTCTGACAAAATCCCATTCCACCCGTACTACTCCCTCAAGGATATCCTGGGTCTAA	300
tra.tem	CTAACTCTGACAAAATCCCATTCCACCCATACTACTCCCTCAAGGATATCCTAGGCCTAA	300
arg.arg	CTAACTCTGACAAAATCCCATTCCACCCATACTACTCCCTCAAGGATATCCTAGGCCTAA	300
cat.wal	CTAAATTCCGACAAAATCCCATTCCACCCCTACTACTCCCTCAAGGACATCCTAGGCCTAA	300
cro.cro	CTAAACTCTGACAAAATCCCATTCCACCCATACTACTCCCTCAAGGATATCCTAGGCCTAA	300
sym.ree	CTAAACTCCGACAAAATCCCATTCCACCCATACTACTCCCTTAAAGACATTCTGGCCTAA	300
bam.cho	CTGACTCTGACAAAATCCCATTCCACCCATACTACACCCCTCAAGGACATCCTAGGCCTAA	300
fra.fra	CTAACTCTGACAAAATCCCATTCCACCCATACTACTCCCTCAAGGATATCCTAGGCCTAA	300
ich.cru	CAAACCTGGATAAAAATCCCATTCCACCCCTATTCTTCTTAAAGGATATCCTAGGATTCA	300
ant.par	CAAACCTGGATAAAAATCCCATTCCACCCCTATTCTTCTTAAAGGATATCCTAGGATTCA	300
ant.vir	CAAACCTGGATAAAAATCCCATTCCACCCCTACTTTCTTAAAGGATATCCTAGGATTCA	300
gru.ant.ant	CAAACCTGGATAAAAATCCCATTCCACCCCTACTTTCTTAAAGGATATCCTAGGATTCA	300
gru.ant.gil	CAAACCTGGATAAAAATCCCATTCCACCCCTACTTTCTTAAAGGATATCCTAGGATTCA	300
gru.ant.shu	CAAACCTGGATAAAAATCCCATTCCACCCCTACTTTCTTAAAGGATATCCTAGGATTCA	300
gru.leu	CAAACCTGGATAAAAATCCCATTCCACCCCTACTTTCTTAAAGGATATCCTAGGATTCA	300
gru.can.pra	CAAACCTGGATAAAAATCCCATTCCACCCCTATTCTTAAAGGATATCCTAGGATTCA	300
gru.can.cow	CAAACCTGGATAAAAATCCCATTCCACCCCTATTCTTAAAGGATATCCTAGGATTCA	300
gru.can.tab	CAAACCTGGATAAAAATCCCATTCCACCCCTATTCTTAAAGGATATCCTAGGATTCA	300
gru.can.san	CAAACCTGGATAAAAATCCCATTCCACCCCTATTCTTAAAGGATATCCTAGGATTCA	300
gru.ame	CAAACCTGGATAAAAATCCCATTCCACCCCTATTCTTAAAGGATATCCTAGGATTCA	300
gru.zsu	CAAACCTGGATAAAAATCCCATTCCACCCCTATTCTTAAAGGATATCCTAGGATTCA	300

gru.mon	CAAACTGCGATAAAAATCCATTCCACCCCTATTTTCTTAAAAGATATCCTAGGATTCA	300
gru.nig	CAAACTGCGATAAAAATCCATTCCACCCCTATTTTCTTAAAAGATACCTAGGATTCA	300
gru.jap	CAAACTGTGATAAAAATCCCATTCCACCCCTATTTTCTTAAAAGATATCTTAGGATTCA	300
cic.boy	CAAACTGCGACAAAAATCCATTCCACCCCTACTTCTCCCTCAAAGATATCTAGGCCTTA	300
rhe.ame	CTCACTCTGACAAAAATCCCATTCCACCCCTACTTCTCCCTAAAAGATGCCCTAGGACTAG	300
ant.alb	CCAACTGCGACAAAAATCCCATTCCACCCCTACTTGCCTAAAAGACATCTAGGATTCA	300
fal.fam	CAAACTGCGATAAAAATCCCATTCCACCCCTATTACTCTCTCAAAGACCTCTAGGATTCA	300
fal.ver	CAAACTGCGACAAAAATCCCATTCCACCCCTACTCTCAAAGACCTTTAGGACTCA	300
fal.per	CAAACTGCGACAAAAATCCCATTCCACCCCTACTCTCAAAGATATCTAGGATTCA	300
fal.spa	CAAACTGTGACAAAAATCCCATTCCACCCCTACTCTCAAAGACCTCTAGGTTTA	300
ayt.ame	CAAACTGCGACAAAAATCCCATTCCACCCCTACTCTCAAAGACATCTAGGATTCA	300
smi.sha	CAGACTGCGACAAAAATCCCATTCCACCCCTACTCTCAAAGACATCTAGGATTCA	300
vid.cha	CTAACTCCGATAAAAATCCCATTCCACCCCTACTTCTCCATAAAAGACATCTAGGTTTG	300
chry.pic	CAGACTGTGACAAAAATCCCATTCCACCCCTACTACACCACAAAGGACATCTAGGCTTCG	300
emy.orb.kur	CAAACACTGACAAAAATCCCATTCCACCCCTATTCTCATATAAAGACCTTTAGGCGTCA	300
che.mud	CAAACACCGATAAAAATCCCATTCCACCCCTACTCTCATAACAAGACCTTTAGGACTCA	300
eum.egr	CAAATACCGACAAAAATCCCATTCCACCCCTACTCTCATAACAAGACCTTTAGGACTCA	300
	CTAGCACAGATAAGGTGCCATTCCACCCCTATTACACATRCAAAGACCTTTGGTTCA	300
	* * *	*
aep.mel	TATTAATAATTCTAGCCTAATACTCCTAGTACTATTCAACCCGACCTACTAGGAGACC	360
ore.ore	TATTAATAATTCTAGCTTTATTACTCTTAGTATTATTCAACACCTGACCTACTTGGAGACC	360
add.nas	TACTACTAATTCTAGCCTCATACTACTAGTACTATTCAACACCCGACCTACTTGGAGACC	360
ory.dam	TACTACTAATTCTAGCCCTTATGTTGCTAGTAATTTCGACCCGACCTACTTGGAGACC	360
hip.equ	TACTACTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTACTTGGAGACC	360
alc.bus	TAATTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC	360
sig.lic	TAATTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC	360
bea.hun	TAATTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC	360
dam.lun	TAATTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC	360
con.tau	TAATTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC	360
amm.ler	TAATTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC	360
pse.nay	TAATTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC	360
cap.ibe	TAATTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC	360
hem.jem	TAATTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC	360
cap.fal	TAATTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC	360
rup.pyr	TAATTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC	360
rup.rup	TAATTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC	360
nem.cau	TAATTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360
bud.tax.tax	TAATTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360
pan.hod	TAATTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360
ovi.amm	TCCTACTAATTCTCACCCTCATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360
ovi.vig	TCCTACTAATTCTCACCCTCATGCTGCTAGTACTATTTCGACCTGACTTGGAGACC	360
cap.cri	TCCTACTAATTCTCACCCTCATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360
ovi.mos	TAATTAATTCTCACCCTTATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360
ore.ame	TAATTAATTCTCACCCTTATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360
cep.dor	TAATTAATTCTCACCCTTATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360
cep.max	TAATTAATTCTCACCCTTATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360
bis.bon	TAATTAATTCTCACCCTTATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360
bos.gru	TAATTAATTCTCACCCTTATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360
bos.tra	TAATTAATTCTCACCCTTATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360
bub.min	TAATTAATTCTCACCCTTATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360
buba.bub	TAATTAATTCTCACCCTTATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360
tra.ang	TAATTAATTCTCACCCTTATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360
tra.eur	TAATTAATTCTCACCCTTATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360
kob.ell	TAATTAATTCTCACCCTTATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360
kob.meg	TCCTATTAACTCCTAATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360
ced.aru	TAATTAATTCTCACCCTTATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360
ced.ful	TAATTAATTCTCACCCTTATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360
nco.moc	TCCTATTAACTCCTAATACTACTAGTACTATTTCGACCTGACTTGGAGACC	360

pel.cap TATTAACCTAACTCTAACACTCCTAGTATTACCCCTGACCTATTAGGACACC 360  
 gaz.dam TACTAATTAACTTAGCCCTCATACTCCTAGTTCTATTACACCCAGATCTGCTTGGAGACC 360  
 our.our TCCTACTAACTTAGCCCTCATGCTCTAGTCCTATTACACCCAGACCTGCTTGGAGACC 360  
 ant.cer TACTAATTAACTAACCCCTCATGCTCTAGTCCTATTACACCCGACCTGCTTGGAGACC 360  
 sai.cat TACTACTTAACTCAATCCTCATACTTCCTAGTCCTATTTCACCCAGACCTGCTTGGAGACC 360  
 mad.kir TACTACTAATTATAGCCCTCATACTCCTAGTTCTATTTCACCCAGACCTGCTTGGAGACC 360  
 rap.mel TCCTATTAACTCTAACCCCTATGCTCTAGTTCTATTTCACCCGACCTACTCGGAGACC 360  
 gaz.gaz TACTACTAACTCTAGTTCTATTACTCCTAGTTCTATTACCCGACCTACTCGGAGACC 360  
 ant.ame TACTAATAACTCTAGCCCTAAATACTAGTACTATTTCACCCAGACCTGTTAGGAGACC 360  
 hyd.ine TCCTCTAACTCTTCTCTAACTGTATTAGTCCTATTTCACCCGACCTGCTTGGAGACC 360  
 mun.mun TACTCTAACTCTTCTCTAACTATTAGTATTATTCTGCTTACCCAGACCTGCTTGGAGACC 360  
 alc.alc TACTCTAACTCTTCTCTAACTACTACTAGTACTCTTCTACCCAGACCTGCTTGGAGACC 360  
 cer.el.a.kan TACTCTAGTACTCTTCTCTAACTACTAGTATTTCACCCGACCTGCTTGGAGACC 360  
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 cer.nip.pul TACTCTAGTACTCTTCTGATATTACTAGTATTTCACCCGACCTGCTTGGAGATC 360  
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 ran.taz TACTCTAACTCTCTCTTAATTAACACTAGTACTATTTCACCCGACCTGCTTGGAGACC 360  
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 tra.jav TAGCCCTATTCTAGCCCTAACTACTAGTCTATTTCACCCGACCTGTTGGAGACC 360  
 trag.nap TAGCTCTAACTACTAGTCTTCTATTACTAGTCTATTTCACCCGACCTGTTGGAGACC 360  
 bala.acu TACTACTAACTCTAACCCCTACTAGCACTAACCCCTATTTCACCCGACCTGCTTGGAGACC 360  
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 esch.rob TACTACTAACTCTAACCCCTACTAACACTAACCCCTATTTCACCCGACCTGCTTGGAGACC 360  
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 mega.nov TATTACTAACTCTAACCCCTACTAACACTAACCCCTATTTCACCCGACCTGCTTGGAGACC 360  
 bala.phy TATTACTAACTCTAACCCCTACTAACACTAACCCCTATTTCACCCGACCTGCTTGGAGACC 360  
 cap.mar TACTACTAACTCTAACCCCTACTAACACTAACCCCTATTTCACCCGACCTGCTTGGAGACC 360  
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 lage.obl TATTCTTAATCTAACCCCTACTAACACTAACCCCTATTTCACCCGACCTGCTTGGAGACC 360  
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 lage.aus TATTCTTAATCTAACCCCTACTAACACTAACCCCTATTTCACCCGACCTGCTTGGAGACC 360  
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 lage.obs TATTCTTAATCTAACCCCTACTAACACTAACCCCTATTTCACCCGACCTGCTTGGAGACC 360  
 lisso.bor TATTCTTAATCTAACCCCTACTAACACTAACCCCTATTTCACCCGACCTGCTTGGAGACC 360  
 lisso.pet TATTCTTAATCTAACCCCTACTAACACTAACCCCTATTTCACCCGACCTGCTTGGAGACC 360  
 glo.mac TACTCTTAATCTTAGCCCTACTAGCACTAACACTAACCCCTATTTCACCCGACCTGCTTGGAGACC 360  
 glo.mel TACTCTTAATCTTAGCCCTACTAGCACTAACACTAACCCCTATTTCACCCGACCTGCTTGGAGACC 360  
 fere.att TACTCTTAATCTAACACTAACACTAACCCCTATTTCACCCGACCTGCTTGGAGACC 360  
 pepo.ele TACTCTTAATCTTAGCCCTACTAGCACTAACACTAACCCCTATTTCACCCGACCTGCTTGGAGACC 360  
 gram.grt TACTCTTAATCTAACACTAACACTAACCCCTATTTCACCCGACCTGCTTGGAGACC 360  
 pse.cra TACTCTTAATCTAACACTAACACTAACCCCTATTTCACCCGACCTGCTTGGAGACC 360  
 lage.acu TACTCTTAATCTAACACTAACACTAACCCCTATTTCACCCGACCTGCTTGGAGACC 360  
 orci.bre TACTCTTAATCTAACACTAACACTAACCCCTATTTCACCCGACCTGCTTGGAGACC 360  
 orca.bre TACTCTTAATCTAACACTAACACTAACCCCTATTTCACCCGACCTGCTTGGAGACC 360

del.cap	TACTCCTAACTTAAACCCCTACTAAGCACTGACCCATTCACTCCAGACCTACTAGGGAGACC	360
del.tro	TACTCCTAACTTAAACCCCTACTAAGCACTGACCCATTCACTCCGGACCTACTAGGGAGACC	360
del.del	TACTCCTAACTTAAACCCCTACTAAGCACTAACCCATTCACTCCGGACCTACTAGGGAGACC	360
sten.cly	TACTCCTAACTTAAACCCCTACTAAGCACTAACCCATTCACTCCCCGACCTACTAGGGAGACC	360
sten.coe	TACTCCTAACTTAAACCCCTACTAAGCACTAACCCATTCACTCCCCGACCTACTAGGGAGACC	360
tur.adu	TACTCCTAACTTAAACCCCTACTAAGCACTAACCCATTCACTCCCCGACCTACTAGGGAGACC	360
sten.fro	TACTCCTAACTTAAACCCCTACTAAGCACTAACCCATTCACTCCCCGACCTACTAGGGAGACC	360
saus.chi	TACTCCTAACTTAAACCCCTACTAAGCACTAACCCATTCACTCCCCGACCTACTAGGGAGACC	360
scen.lon	TACTCCTAACTTAAACCCCTACTAAGCACTAACCCATTCACTCCCCGACCTACTAGGGAGACC	360
turs.tru	TACTCCTAACTTAAACCCCTACTAAGCACTAACCCATTCACTCCCCGACCTACTAGGGAGACC	360
lage.alb	TACTTTAACTCTAAACCCCTACTAAGCACTAACCCATTCACTCCCCGACCTACTAGGGAGACC	360
sten.bre	TACTTTAACTCTAACTTTACTAGCACTAACCCATTCACTCCCCGACCTACTAGGGAGACC	360
sota.flu	TACTCCTAACTCTGACCCCTACTAAGCACTAACCCATTCACTCCCCGACCTACTAGGGAGACC	360
del.leu	TACTACTAACTCTAAACCCATTAAACAGTRACCCATTCAACCTGACCTCTAGGGAGACC	360
mono.mon	TCTTACTAACTCTAAATTCACTAGCAATAACCCCTACTCACACCTGACCTCTAGGGAGACC	360
plat.gan	TGATCCTAACTCTAAACCTCACTCACATTAAACCTTATTACACCTGACCTACTAGGGAGACC	360
plat.min	TGATCCTAACTCTAAACCTCACTCACATTAAACCTTATTACACCTGACCTACTAGGGAGACC	360
kogi.bre	TACTGCTAACTCTGCGCTACTTACATTAAACCCATTTCGCACCRGACCTATTAGGGAGACC	360
kogi.sim	TACTACTAACTCTGCGCTACTTACACTCACAGTACCCCTTTGGCACCTGACTACTAGGGAGACC	360
phys.cat	TACTACTAACTCTTACCCCTACTTACACTAACCCCTTTGGCACCCGACCTGCTAGGGAGACC	360
lipo.vex	TTCTTATTAAATTTGTCTACTCACACTAACCTTACTTGCAACAGACCTACTCGGAGATC	360
phoc.sin	TACTATTAACTTCTAACTTACTAACACTAACCTTATTTCGACCTCTAGGGAGACC	360
bera.bai	TACTACTAACTCTAGCCCTACTCAGCCTAACCCATTTCGCACCCGACCTACTAGGGAGACC	360
ziph.car	TACTATTAACTCTGCTACTTACCTAACCCCTTTCGCACCCGACCTGCTAGGGAGACC	360
meso.eur	TACTACTAACTCTGCTACTTACCTAACCCCTTTCGCACCCGACCTGCTAGGGAGACC	360
meso.bid	TACTACTAACTCTGCGCTACTTACCTAACCCCTTTCGCACCTGACTACTAGGGAGACC	360
meso.den	TACTATTAACTCTGCCCTACTTACCTAACCCCTTTCGCACCCGACCTACTAGGGAGACC	360
hype.amp	TATTACTAACTCTAGCTCTACTCACATTAAACCCCTTTCGCACCTGACTATTAGGGAGACC	360
meso.per	TATTATTAAATTAGTCTACTTACCTAACCCCTTTCGCACCCGACCTTTCGACCTATTAGGGAGACC	360
pent.bla	TATTAATTAACTCTAACATAACTCACGCTGACTCTTACCTAACCCCTTTCGCACCTCTAGGGAGACC	360
hex.lib	TACTTCTAACTACAATAACTCACACTAACCTTATTGGCACCTGACCTACTAGGGAGACC	360
hipp.amp	TACTCCTAACTAACACACTCACACTAACCTTATTGGCACCTGACCTACTAGGGAGACC	360
dic.sum	TACTTCTAACTCTAGCCCTACTCACCTAACCCCTTTCGCACCTGACTACTAGGGAGACC	360
rhin.sch	TGTTCTAAATTAGTACTTACCTAACCCCTTTCGCACCTGACTACTAGGGAGACC	360
cera	TACTCCTAACTCTAGCCTACTCGCCCTAGTTCTATTTCGCACCTGACTACTAGGGAGACC	360
equu	TCTCTCTACTCTACTCTACTAACCCCTAGTATTCTATTTCGCACCTGACTACTAGGGAGACC	360
baby.bab	TACTCATATTAACTAGCTCTTAATCTACTAACCCCTTTCGCACCTGACTACTAGGGAGACC	360
ptac.afr	TATTGATAACTAACTCTACTAACCCCTACTAACCTGACTTAACTAACCCCTTTCGCACCTGACTACTAGGGAGACC	360
sus.bar	TATTGATAACTAACTCTACTAACCCCTACTAACCTGACTTAACTAACCCCTTTCGCACCTGACTACTAGGGAGACC	360
sus.scr.ewb3	TATTGATAACTAACTCTACTAACCCCTACTAACCTGACTTAACTAACCCCTTTCGCACCTGACTACTAGGGAGACC	360
lama.gla	TACTACTTAACTCTAACCCCTACTTCTACTAACCTGACTTAACTAACCCCTTTCGCACCTGACTACTAGGGAGACC	360
lama.gua	TACTACTTAACTCTAACCCCTACTTCTACTAACCTGACTTAACTAACCCCTTTCGCACCTGACTACTAGGGAGACC	360
vic.vic	TACTACTTAACTCTAACCCCTACTTCTACTAACCTGACTTAACTAACCCCTTTCGCACCTGACTACTAGGGAGACC	360
cam.bac	TGCTACTAACTAAATTCTGCTTATTCTGACTTAACTAACCCCTACTAACCTGACTACTAGGGAGACC	360
arc.for	TCCTACTAACTCTGATTCTACTAACCCCTACTTCTGACTTAACTAACCCCTACTAACCTGACTACTAGGGAGACC	360
arc.gaz	TCTTACTAACTCTGATTCTACTAACCCCTACTTCTGACTTAACTAACCCCTACTAACCTGACTACTAGGGAGACC	360
eum.jub	TCCTACTAACTCTGATTCTACTAACCCCTACTTCTGACTTAACTAACCCCTACTAACCTGACTACTAGGGAGACC	360
sal.cal	TCCTACTAACTCTGATTCTACTAACCCCTACTTCTGACTTAACTAACCCCTACTAACCTGACTACTAGGGAGACC	360
odo.zes	TCCTACTAACTCTGATTCTACTAACCCCTACTTCTGACTTAACTAACCCCTACTAACCTGACTACTAGGGAGACC	360
pho.associata	TACTCTCATCTAACTAACCCCTACTTCTACTAACCCCTACTTCTGACTTAACTAACCCCTACTAACCTGACTACTAGGGAGACC	360
pho.gro	TACTCTCATCTGCTGCTTAACTAACCCCTACTTCTACTAACCCCTACTTCTGACTTAACTAACCCCTACTAACCTGACTACTAGGGAGACC	360
pho.vic	TACTCTCATCTGCTGCTTAACTAACCCCTACTTCTACTAACCCCTACTTCTGACTTAACTAACCCCTACTAACCTGACTACTAGGGAGACC	360
cys.cci	TACTCTCATCTGCTGCTTAACTAACCCCTACTTCTACTAACCCCTACTTCTGACTTAACTAACCCCTACTAACCTGACTACTAGGGAGACC	360
hyd.leg	TACTCTCATCTGCTGCTTAACTAACCCCTACTTCTACTAACCCCTACTTCTGACTTAACTAACCCCTACTAACCTGACTACTAGGGAGACC	360
leg.wed	TACTCTCATCTGCTGCTTAACTAACCCCTACTTCTACTAACCCCTACTTCTGACTTAACTAACCCCTACTAACCTGACTACTAGGGAGACC	360
ris.leo	TACTCTCATCTGCTGCTTAACTAACCCCTACTTCTACTAACCCCTACTTCTGACTTAACTAACCCCTACTAACCTGACTACTAGGGAGACC	360
rii.but	TACTCTCATCTGCTGCTTAACTAACCCCTACTTCTACTAACCCCTACTTCTGACTTAACTAACCCCTACTAACCTGACTACTAGGGAGACC	360
ton.rich	TACTCTCATCTGCTGCTTAACTAACCCCTACTTCTACTAACCCCTACTTCTGACTTAACTAACCCCTACTAACCTGACTACTAGGGAGACC	360

hela.mal	TACCTCTTACCCCTAACAAACCCTAGTTCTATTCTCGCCCCGACTTACTAGGAGACC	360
sel.chi	TACCTCTCATCCTTACCCCTAACAAACCCTAGTTCTATTCTCGCCCCGACTTACTAGGAGACC	360
ail.ful	TACTCCTTATCCTAATTCTCATGACATTAGTACTATTCCTTGACTTGTGGATC	360
fel	TAGTACTAGTTAACACTCATACTACTCGCTCTATTTCACCCAGACCTGCTAGGAGACC	360
can	TACTCCTACTCCTAACCTTAATACTCACTAGTTTATTTCACCTGACCTTATTAGGAGACC	360
tal	TAATCCTAATTATAGCTCTATCATCATAGTATTATTCACCTGACCTACTACOAGACC	360
gia.sab	TAATCCTCATCTTAATCTCATAACCCCTAGTTCTTCACCCCGATCTTAGGAGACC	360
gia.vol	TAATCCTTATCTTAATCTCATAACCCCTAGTTCTTCACCCCGATCTTAGGAGACC	360
byl.pha	TTATTCCTTCTCTTAACTTTTATAAACTTACTAGTACTATTTCCCCGATTTAGGAGACC	360
pet.sec	TTATTCCTTCTCTTAACTTTTATAAACTTACTAGTACTATTTCCCCGATTTAGGAGACC	360
bal.pea	TAATCCTAACCCCTATATTACAAACCCCTATTCTATTCCCGCCCTGATCTCTAGGAGACC	360
pce.mcm	TTCTCCCTGGCCTCTTATTCTATACTTACTCTCTTACTCCAGACCTCCTTGAGACC	360
gala.demi	TTATTCCTTACTAACTCTGTTCTCCCTAGTAATTCTCCCCGGACCTGCTAGGAGACC	360
pero.pct	TCTTCTTCTACTAACCTACTAACCCCTAGCTATTCTCCCCGACCTTATTAGGAGACC	360
gala.mat	TCTTCTTACTACTATGCCATTCTCTCTAGTACTATTTCCCCGATCTTAGGAGACC	360
gala.moh	TCCTCTTACTATTATGCCATTCTCTCTAGTACTATTTCTCCCCGACCTGCTGGAGACC	360
oco.gar	TCCTCCCTTCTAACCCCTATTCTCCCTAGTACTATTCTCCCCGACCTTTAGGAGACC	360
lor.taz	TTGCTCTTAAATGCCCTTCTAACTCTAGTCTTATTCTCCCGTACCTCTAGGAGACC	360
nyc.cou	TTTCCTTATTAGCAACCCCTATCTATTCTAGTCTTATTCTCCCGTACCTCTAGGAGACC	360
mus	TAATCCTATTCTTATTCTCATAACCCCTAGTATTATTTCCAGACCTACTAGGAGACC	360
gorz	TCCTCTTCTGACCTTGTATAACCTATTCTACCCAGACCTCTAGGAGACC	360
homo	TTCTCTTCTTCTCTCTTAATGACATTAACCTATTCTACCCAGACCTCTAGGAGACC	360
dug.dug	TCCTCTCATCTAGCTTACTCTCTAACCCCTTTCTCCCCGGACCTACTGGGAGACC	360
ele.max	TTATCCTATTCTACTCCTTCTACTCTAGCCCTACTCTCCAGACCTACTAGGAGACC	360
afr.con	CACTCTGCTCATTCGATTCTGACACTAGCCCTACTCTCCCCCRACTCTTAGGTGATC	360
pavo.mut	CTCTTCTTATTCTACCCATTCTAACCTAGCCCTATTCTCCCCCRACTCTTAGGTGACC	360
tra.bly	CACTCTGCTCACCCCGCTCTCACCTAGCATTATTCTACCCGAACCTTATTAGGGGACC	360
tra.sac	CACTCTGCTCACCCCGCTCTCACCTAGCCCTATTCTACCCAAACCTACTAGGTGATC	360
tra.cob	CACTCTACTCTCTCTCACCTAGCCCTATTCTACCCAAACCTACTAGGTGACC	360
tra.tem	CACTCTACTCGCTCCATTCTTACACTTACCCCTATTCTACCCAAACCTACTAGGTGACC	360
arg.arg	CACTTATACTACCCCGCTCTAACACTAGCCCTATTCTACCCAAACCTTCTGGGGGACC	360
cat.wal	CACTTATACTACCCCGCTCTAACACTAGCCCTATTCTACCCAAACCTACTAGGTGACC	360
cro.cro	CACTTATACTACCCCGCTCTCACACTAGCCCTATTCTACCCAAACCTACTAGGTGACC	360
sym.ree	CACTTATACTACCCCGCTCTCACACTAGCCCTATTCTACCCAAACCTACTAGGTGACC	360
bam.cho	CCCTTATACTACCCCGCTCTTACACTAGCCCTATTCTACCCAAACCTTCTGGGGGACC	360
fra.fra	CACTTATACTACCCCGCTCTTACACTAGCCCTATTCTACCCAAACCTTCTAGGAGACC	360
ich.cru	TACTCATACTACTCCCCTACTCATAACCTTAGCTCTATTCTACCCAAACTTACTAGGAGACC	360
ant.par	TACTCATACTACTCCCCTACTCATAACCTTAGCTCTATTCTACCCAAACTTACTAGGAGACC	360
ant.vir	TACTCATACTACTCCCCTACTCATAACCTTAGCTCTATTCTACCCAAACCTACTAGGAGACC	360
stu.ant.ant	CACTCATACTACTCCCCTACTCATAACCTTAGCTCTATTCTACCCAAACCTACTAGGAGACC	360
stu.ant.gil	CACTCATACTACTCCCCTACTCATAACCTTAGCTCTATTCTACCCAAACCTACTAGGAGACC	360
stu.ant.sha	CACTCATACTACTCCCCTACTCATAACCTTAGCTCTATTCTACCCAAACCTACTAGGAGACC	360
stu.leu	TACTCATACTACTCCCCTACTCATAACCTTAGCTCTATTCTACCCAAACCTACTAGGAGACC	360
stu.can.pra	TACTCATACTACTCCCCTACTCATAACCTTAGCTCTATTCTACCCAAACCTACTAGGAGACC	360
stu.can.sow	TACTCATACTACTCCCCTACTCATAACCTTAGCTCTATTCTACCCAAACCTACTAGGAGACC	360
stu.can.tab	TACTCATACTACTCCCCTACTCATAACCTTAGCTCTATTCTACCCAAACCTACTAGGAGACC	360
stu.can.can	CACTCATATTACTCCCCTACTCATAACCTTAGCTCTATTCTACCCAAACCTACTAGGAGACC	360
stu.ame	TACTCATATTACTCCCCTACTCATAACCTTAGCTCTATTCTACCCAAACCTACTAGGAGACC	360
stu.gru	TACTCATATTACTCCCCTACTCATAACCTTAGCTCTATTCTACCCAAACCTACTAGGAGACC	360
stu.mon	TACTCATATTACTCCCCTACTCATAACCTTAGCTCTATTCTACCCAAACCTACTAGGAGACC	360
stu.nig	TACTCATATTACTCCCCTACTCATAACCTTAGCTCTATTCTACCCAAACCTACTAGGAGACC	360
stu.jap	CACTCATATTACTCCCCTACTCATAACCTTAGCTCTATTCTACCCAAACCTACTAGGAGACC	360
cic.boy	CACTCTACTCTCCACTAACCTAGCTCTATTCTACCCAAACCTACTAGGTGACC	360
che.ame	CTCTCATATTCTACCCCTACTCATAACCTTAGCTCTATTCTACCCAAACCTACTAGGAGACC	360
ant.alb	CACTAATACTCCCTCTAACCTCTAACCTTAGCTCTATTCTACCCAAACCTACTAGGAGACC	360
ail.sam	TACTCATATACTTCTAACCTTAGCTCTATTCTACCCAAACCTACTAGGAGACC	360
ail.vuc	TACTCATATACTTCTAACCTTAGCTCTATTCTACCCAAACCTACTAGGAGACC	360
ail.pet	TACTCATATACTTCTAACCTTAGCTCTATTCTACCCAAACCTACTAGGAGACC	360

fal.spa	TGCTCATACTCTGCCCTAAATAGCCCTAGCCCTATTCAACCCCCAACCTGCTAGGAGACC	360
ayt.ame	TCCTCATGTCACCCCCCTAAATAGCACTAGCCCTATTCTCACCAAAACCTCTAGGAGACC	360
smi.sha	CAATCATACTAACACCACTAAACCCCTAGCCATATTCTCTCTAACCTCTAGGAGACC	360
vid.cha	TACTAATATTCGGCACTCTAGCTTCACTAGCCCTATTCTCCCCAACATACTAGGAGATC	360
chry.pic	TTCTAATACTAACCCCTCTACTAACCCCTAACACTATTCTCTCCAAACCTTTAGGGGACC	360
emy.orb.kur	TCCTAATACTAGCCCTCTGCTAACCCCTAACACTATTCTCTCTAACCTCTAGGAGACC	360
che.mud	TTTTAATACTAACCTTCTCTAACCTAACACTTTCTCCCCACTTACTAGGAGACC	360
eum.egr	TCATTATACTGTCTGTTCTACTAGCCCTCGCCCTTTCTCACCAAAACCTCTAGGGGACC	360
* * * * *		
aep.mel	CAGACAAANNACATCCCCGCAAACCCACTCAACACCCCTCCCCACATCAAGCCCGAATGGT	420
ore.ore	CAGATAACTACACCCCGCAAACCCACTCAACACACTCCCCCTCACATTAAACCGAGAATGGT	420
add.nas	CAGACAATTATAACCCCGCAAATCCACTTAGCACGCCCTCACATCAAAACCTGAATGAT	420
ory.dam	CAGATAATTATAACCCAGCAAATCCACTTAACACACCCCTCACATCAAAACCCGAATGAT	420
hip.equ	CAGACAACTATGCCCTCGCAAACCCACTCAACACGGCCCTCACATTAAACCGAGTGT	420
alc.bus	CAGACAACTACACCCCGCGAACCCACTTTAACACACCCCTCACATCAAGCCCGAATGAT	420
sig.lic	CAGACAACTACACCCCGCGAACCCACTTTAACACACCCCTCACATCAAAACCCGAATGAT	420
bea.hun	CAGACAACTACACCCCGCGAACCCACTTTAACACACCCCTCACATCAAGCCCGAATGAT	420
dam.lun	CAGACAACTACACCCCTGCAAACCCACTCAACACACCCCTCACATCAAGCCCGAATGAT	420
con.tau	CAGACAACTACACCCCGCGAACCCACTCAACACACCCCTCACATCAAAACCTGAATGAT	420
amm.ler	CAGACAACTATAACCCCGCGAACCCACTCAACACACCCCTCACATCAAAACCTGAATGAT	420
pse.nay	CAGACAACTACACCCCGCGAACCCACTCAACACACCCCTCACATCAAAACCCGAATGAT	420
cap.ibe	CAGACAACTATAACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
bem.jem	CAGACAACTATAACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAGTGGT	420
cap.fal	CAGATAACTATATCCCAGCAAATCCACTCAACACACCCCTCATATTAAACCTGAATGAT	420
rup.pyr	CAGATAACTATACCCCGCGAACCCACTCAACACACCCCTCACATCAAAACCCGAATGAT	420
rup.rup	CAGACAACTATAACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
nem.cau	CAGACAACTATAACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
bud.tax.tax	CAGACAACTATAACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
paz.hod	CAGACAACTACACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
ovi.arm	CAGACAACTACACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
ovi.vig	CAGACAACTACACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
cap.cri	CAGACAACTACACTCCAGCAAACCCACTCAACACACCCCTCACATCAAGCCCGAGTGT	420
ovi.mos	CAGACAACTATAACCCCGCGAACCCACTCAACACACCCCTCACATTAAACAGAGTGT	420
ore.ame	CAGACAACTACACTCCAGCAAACCCGCTAAATACACCTCCCCATATCAAGCCCGAATGAT	420
cep.dor	CAGACAACTACACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
cep.max	CAGACAACTATAACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
bis.bon	CAGACAACTACACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
bos.gru	CAGACAACTACACCCCGCGAACCCACTCAACACACCCCTCACATTAAAGCCCGAATGAT	420
bos.tra	CAGACAACTACACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
bub.min	CAGACAACTACACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
buba.bub	CAGACAACTACACCCCGCGAACCCACTCAACACACCCCTCACATTAAAGCCTGAATGAT	420
tra.ang	CCGACAACTACACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
tra.eur	CCGACAACTACACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
kob.ell	CTGACAACTATGCCCTCGCAAACCCACTTAACACGCCCTCACATTAAACCTGAATGAT	420
kob.meg	CTGACAACTATAACCCCGCGAACCCACTTAACACACCCCTCACATTAAACCTGAATGAT	420
red.aru	CCGACAACTATAACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
red.ful	CCGACAACTATAACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
neo.mos	CAGACAACTACACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
pel.cap	CTGACAACTACACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
gaz.dam	CAGACAACTACACCCCGCGAACCCACTCAACACACCCCTCACATTAAAGCCTGAATGAT	420
our.our	CAGACAACTATAACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
anz.cer	CAGACAACTATAACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
sai.tat	CAGACAACTACACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
mad.kir	CAGACAACTACACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
rap.mel	CAGACAACTATAACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
gaz.gaz	CAGACAACTATAACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420
ant.ame	CCGACAACTACACCCCGCGAACCCACTCAACACACCCCTCACATTAAACCTGAATGAT	420

turs.tru	CTGATAACTACACCCAGCAAACCCACTAAGCACCCTGCACACATCAAACCGAGAATGAT	420
lage.alb	CCGATAACTATACCCAGCAAATCCACTAAGCACTCCTGCACACATCAAACCGAGAATGAT	420
scen.bre	CCGACAACATACCCAGCAAATCCACTAAGCACCCTGCACACATCAAACCGAGAATGAT	420
sota.flu	CCGACAACATACTCCAGCAAATCCACTAACACCCCTGCACACATCAAACCGAGAATGAT	420
del.leu	CAGACAATTACACCCAGCAAACCCACTAAACACCCCCGCACACATCAAACCGAGAATGAT	420
mono.mon	CTGACAATTATACCCAGCAAACCCACTAAGCACCCTGCACACATCAAACCGAGAATGAT	420
plat.gan	CCGATAACTACACCCAGCAAACCCCTTAATACCCAGCACATATCAAACCGAGGTGAT	420
plat.min	CCGATAACTACACCCAGCAAACCCCTTAATACCCAGCACATATCAAACCGAGGTGAT	420
kogi.bre	CTGACAACATACCCAGCAAACCCACTAAGCACCCTGCACACATCAAACCGAGAATGAT	420
kogi.sim	CCGACAACATACCCAGCAAACCCCTTAATACCCAAACACACATCAAACCGAGAATGAT	420
phys.cat	CTGACAACATACCCAGCAAACCCACTAAACACTCCGGCACACATCAAACCGAGAATGAT	420
lipo.vex	CTGATAATTATACCCAGCAAACCCACTAAACACTCCGGCACACATCAAACCGAGAATGAT	420
phoc.sin	CCGATAACTACATTCCAGCAAACCCACTAAACACTCCGGCACACATCAAACCGAGAATGAT	420
bera.bai	CCGACAACATACCCGGCAAACCCACTAAACACTCCGGCACACATCAAACCGAGAATGAT	420
ciph.car	CCGACAACATACCCAGCAAACCCACTAAACACTCCGGCACACATCAAACCGAGAATGAT	420
meso.eur	CCGACAATTACACCCAGCAAACCCACTTAATACCTCCAGCACACATCAAACCGAGAATGAT	420
meso.bid	CCGACAATTACACCCAGCAAACCCACTCAGCACCCCAGCACACATCAAACCGAGAATGAT	420
meso.den	CCGACAATTATACCCAGCAAACCCACTCAACACTCCAGCACACATCAAACCGAGAATGAT	420
hype.amo	CTGACAACATACCCAGCAAACCCACTCAGCACCTCCAGCACACATCAAACCGAGAATGAT	420
meso.per	CTGACAATTACACTCCAGCAAACCCACTTAGCACCCAGCACATAATTAACCGAGAATGAT	420
pont.bla	CAGACAACATATCCAGCAAACCCATGAATAACCCAGAGCACATTAACCGAGAATGAT	420
hex.lib	CAGACAACATACCCCGCAAACCCCTTAGCACACCACACATCAAACCGAGAATGAT	420
hipp.amp	CAGACAACATACCCCGCAAACCCCTTAGCACACCACACATCAAACCGAGAATGAT	420
dic.sum	CCGACAACATACACCCGCCAACCCCTCTAGCACCCCTCACACATCAAACCGAGAATGAT	420
rhin.son	CAGACAACATACCCAGCAAACCCACTAAACACTCCAGCACACATCAAACCGAGAATGAT	420
cera	CTGACAACATACCCCTGCCAATCTCTCACACTCCCCCACATATCAAACCGAGAATGAT	420
equu	CAGACAACATACCCAGCTAACCCCTCAGCACCTCCATATTAAGCCAGAATGAT	420
baby.bab	CCGACAACATACTCCAGCAAACCCACTAAACACCCACCCACATCAAACCGAGAATGAT	420
phac.aff	CAGACAACATACCCAGCAAACCCACTAAACACCCACCCCATATTAAACCGAGAATGAT	420
sus.bar	CAGACAACATACCCAGCAAACCCACTAAACACCCACCCCATATTAAACCGAGAATGAT	420
sus.scr.ewb3	CCGACAACATACTCCAGCAAACCCACTAAACACCCACCCCATATTAAACCGAGAATGAT	420
lama.gla	CCGACAACATACTCCAGCTAACCCCTCAACACCCGGCCCATATTAAACCGAGAATGAT	420
lama.gua	CCGACAACATACTCCAGCTAACCCCTCAACACCCGGCTCATATTAAACCGAGAATGAT	420
vic.vic	CCGACAACATACCCCGCTAACCCCTTAACACACCACCCACATATTAAACCGAGAATGAT	420
cam.bac	CTGACAACATACTCCAGCTAACCCCTCAATACACCACACACATATTAAAGCCGGAATGAT	420
arc.for	CAGACAACATACCCAGCAAACCCACTAAACACCCACCCCATATTAAACCGAGAATGAT	420
arc.gaz	CAGACAACATACCCAGCAAACCCACTAAACACCCACCCCATATTAAACCGAGAATGAT	420
eum.jub	CAGACAACATACCCAGCAAACCCACTAAACACCCACCCCATATTAAACCGAGAATGAT	420
zal.cal	CCGACAACATACTCCAGCTAACCCCTCAACACCCGGCCCATATTAAACCGAGAATGAT	420
odo.ras	CAGACAACATACCCAGCTAACCCCTCACTACTCCACACATATTCAAACCTGAATGAT	420
pho.fasciata	CAGACAACATACCCAGCTAACCCCTCACTACTCCACACATATTCAAACCTGAATGAT	420
pho.gro	CAGACAACATACCCAGCTAACCCCTCACTACTCCACACATATTCAAACCTGAATGAT	420
pho.vit	CAGACAACATATCCAGCTAACCCCTCAGCACCTCCACACATATTCAAACCTGAATGAT	420
cys.cri	CCGACAACATACCCCTGCCAACCCCTTAAGCACCCACACATATCAAACCCGAATGAT	420
hyd.lep	CCGACAACATACCCCTGCCAACCCCTTAAGTACCCACACATATCAAACCCGAATGAT	420
lep.wed	CCGACAACATATCCCTGCCAACCCCTTAAGCACCCACACATATCAAACCCGAATGAT	420
mir.leo	CCGACAACATACCCCTGCCAACCCCTTAAGCACCCACACATATTAAACCCGAATGAT	420
eri.bar	CCGACAACATACCCCTGCCAACCCCTTAAGCACCCACACATATTAAACCCGAATGAT	420
non.sch	CCGACAACATACCCCTGCCAACCCCTTAAGTACCCACACATATCAAACCCGAATGAT	420
vel.mal	CCGACAACATACCCCTGCCAACCCCTTAAGCACCCACACATATTAAACCCGAATGAT	420
vel.chi	CTGACAACATACCCCTGCCAACCCCTTAAGCACCCACACATATTAAACCCGAATGAT	420
vil.ful	CTGACAACATACCCCTGCCAACCCCTTAAGTACCCACACATATTCAAACCCGAATGAT	420
lei	CTGACAACATATCCCTGCTAACCCCTTAAGCACCCACACATATTAAACCCGAATGAT	420
tan	CAGACAACATACCCCTGCCAACCCCTTAACACCCCTCACACATATTAAACCCGAATGAT	420
ai	CAGACAACATACCCCTGCCAACCCCTTAACACCCCTCACACATATTAAACCCGAATGAT	420
la.sib	CAGACAACATACCCCTGCCAACCCCTTAACACCCCTCACACATATTAAACCCGAATGAT	420
la.vol	CAGACAACATACCCCTGCCAACCCCTTAACACCCCTCACACATATTAAACCCGAATGAT	420
yl.phu	CTGACAACATACCCCTGCCAACCCCTTAACACCCCTCACACATATTAAACCCGAATGAT	420

aep.mel	ACTTCCTGTTNGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
ore.ore	ATTTCTATTNGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
add.nas	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
ory.dam	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
kip.equ	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
alc.bus	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
sig.lic	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
bea.hun	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
dam.lun	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACGGACTAGGAGG	472
con.tau	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
amm.lev	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAAGCTAGGAGG	472
pse.nay	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGGGG	472
cap.ibe	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
hem.jem	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
cap.fal	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
rup.pyr	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
rup.rup	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
nem.cau	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
bud.tax.tax	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
pan.hod	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
cvi.amm	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
cvi.vig	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
cap.cri	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
cvi.mos	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
ore.ame	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
cep.dor	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
cep.max	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
bis.bcn	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
bos.gru	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
bos.tra	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
bub.min	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
buba.bub	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
tra.ang	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
tra.eur	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
kob.ell	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
kob.meg	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
red.aru	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
red.ful	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
neo.mos	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
pel.cap	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
gaz.dam	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
our.out	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
ant.cet	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
sai.zae	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
mad.kit	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
cap.mel	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
gaz.gaz	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
anc.ame	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
hyd.ina	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
mun.mun	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
alc.alc	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
cer.elia.kan	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
cer.elia.kan	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
cer.elia.ca	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
cer.nip.ctac	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
cer.nip.yes	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
cer.nip.ker	ATTTCTATTGCAATCCCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472

cer.nip.pul	ATTTCTTATTGGCATACGCAATCCTACCGATCAATTCCAAACAAAC. AUGAGG	472
cer.nip.nip	ATTTCTTATTGGCATACGCAATCCTACCGATCAATTCCAAACAAACTAGGGAGG	472
cer.elo.sco	ATTTCTTATTGGCATACGCAATCCTACCGATCAATTCCAAACAAACTAGGGAGG	472
cer.dam	ACTTCCTATTGGCATACGCAATCCTACCGATCAATTCCAAATAAAATTAGGGAGG	472
ran.tar	ACTTCCTATTGGCATACGCAATCCTACCGATCAATTCCAAATAAAACTAGGGAGG	472
mos.fus	ATTTCTTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAACTAGGGAGG	472
mos.leu	ATTTCTTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAACTAGGGAGG	472
mos.chr	ATTTCTTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAACTAGGGAGG	472
mos.ber	ATTTCTTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAACTAGGGAGG	472
mos.mes	ATTTCTTATTGGCATATGCCATTCTACCGATCAATTCCAAATAAAACTAGGGAGG	472
tra.jav	ATTTCTTATTGGCATACGCAATTCTCCGTCAATTCCAAATAAAATTAGGGAGG	472
trag.nap	ATTTCTTATTGGCATACGCAATTCTACCGATCAATTCCAAATAAAACTAGGGAGG	472
bala.acu	ATTTCTTATTGGCATACGCAATTCTACCGATCAATTCCAAATAAAACTAGGGGG	472
bala.bon	ATTTCTTATTGGCATACGCAATTCTACCGATCAATTCCAAACAAATTAGGGGG	472
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esch.rob	ATTTCTTATTGGCATACGCAATTCTACCGATCAATTCCAAACAAATTAGGGGG	472
bala.mus	ATTTCTTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAATTAGGGGG	472
mega.zov	ATTTCTTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAATTAGGGGG	472
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cap.mar	ACTTCCTATTGGCATATGCCATTCTACCGATCAATTCCAAATAAAACTAGGGGG	472
ceph.com	ACTTCCTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAATTAGGGGG	472
ceph.eut	ACTTCCTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAATTAGGGGG	472
lage.ovl	ACTTCCTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAATTAGGGGG	472
ceph.haa	ACTTCCTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAATTAGGGGG	472
ceph.hec	ACTTCCTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAATTAGGGGG	472
lage.aus	ACTTCCTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAATTAGGGGG	472
lage.cru	ACTTCCTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAATTAGGGGG	472
lage.obs	ACTTCCTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAATTAGGGGG	472
lisso.bor	ACTTCCTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAATTAGGGGG	472
lisso.per	ACTTCCTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAATTAGGGGG	472
glo.mac	ACTTCCTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAATTAGGGGG	472
glo.mel	ACTTCCTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAATTAGGGGG	472
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lage.acu	ACTTCCTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAACTTGGAGG	472
orsi.bre	ACTTCCTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAACTTGGAGG	472
orca.bre	ACTTCCTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAACTTGGGGG	472
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del.tro	ACTTCCTATTGGCATATGCCATTCTACCGATCAATTCCAAACAAACTTGGAGG	472
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mono.mon	ACTTCCTATTGGCATACGCAATTCTACCGATCAATTCCAAACAAACTTGGAGG	472
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plac.min	ACTTCCTATTGGCATACGCAATTCTACCGATCAATTCCAAACAAACTTGGAGG	472
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 mun.mun CCGACAAATTATACCCCAGCAAACCCACTCAATACACCCCCCTCACATCAAGCCTGAATGAT 420  
 alc.alc CAGACAACTACACCCCCAGCTTAATCCACTCAACACACCCCCCTCATATTAAAGCCTGAATGAT 420  
 cer.elo.kan CAGACAACTATAACCCCAGCAAATCCACTCAATACACCCCCCTCACATTAAACCTGAATGAT 420  
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 pepo.ele CTAACAACCTATAACCCCAGCAAACCCACTCAACACATCAACCGAGGTGGT 420  
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 sten.fro CAGACAACTATAACCCCAGCAAATCCCCTCAGCACCCCCAGCACACATCAACCGAGGTGGT 420  
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phoc.sin	ATTTCTCTTCGCATAACGCAATTCTACGATCAATTCCAATAAACTAGGAGG	472
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ziph.car	ACTTCTATTGCATAACGCAATTCTACGATCAATTCCAATAAACTAGGAGG	472
meso.eur.	ACTTCTATTGCATAACGCAATTCTACGATCAATTCCAACAAACTAGGAGG	472
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pont.bla	ATTTCTATTGCATAACGCAATTCTACGATCAATTCCAATAAACTGGGAGG	472
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hipp.amp	ATTTCTATTGCATAATGCAATTCTACGATCAATTCCAATAAACTAGGAGG	472
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cera	ATTTCTGTTGCCATTGCCATCCTACGATCAATTCCAACAAACTAGGAGG	472
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sus.scr.ewb3	ATTTCTATTGCCATTGCCATCCTACGCTATTCTACGTTCAATTCCAATAAACTAGGTGG	472
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hela.mal	ATTTCTATTGCCATTGCCATCCTACGATCTATCCAACAAACTAGGAGG	472
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homo	ATTTCTATTGCCATACACATTCTCCGATCCGTCCCTAACAAACTAGGAGG	472
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cro.cro	ACTTCCTATTGCCATACGCCATTCTACGCTCAATCCCCAACAAACTGGGGG	472
sym.ree	ACTTCCTATTGCCATACGCCATTCTACGCTCAATCCCCAACAAACTCGGAGG	472
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fra.fra	ACTTCCTATTGCCATACGCTATTCTACGCTCAATCCCCAACAAACTCGGAGG	472
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ant.par	ACTTCCTATTGCCATACGCTATTCTACGCTCAATCCCCAACAAACTAGGAGG	472
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fal.per	ATTTCTATTGCCATTACGCCATTCTACGTTCAATCCCCAACAAACTAGGAGG	472
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smi.sha	ATTTCTATTGCCATTACGCCATTCTACGTTCAATCCCCAACAAACTAGGAGG	472
vid.cha	ATTTCTATTGCCATTACGCCATTCTACGTTCAATCCCCAACAAACTAGGAGG	472
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emy.orb.kuc	ATTTCTTTGCCATTACGCCATTCTACGTTCAATCCCCAACAAACTAGGAGG	472
che.mud	ATTTCTATTGCCATTACGCCATTCTACGTTCAATCCCCAACAAACTAGGAGG	472
eum.egg.	ATTTCTATTGCCATTACGCCATTCTACGTTCAATCCCCAACAAACTAGGAGG	472
PRIMER 'mcb869'	CGATCAATCCCCAACAAACTAGGAGG	

\* \* \* \* \*

Results for RID 984593689-1224-27770



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997). "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593689-1224-27770

Query=

(328 letters)

Database: Sequences from complete mitochondrial genomes  
129 sequences; 3,164,247 total letters

If you have any problems or questions with the results of this search  
please refer to the BLAST FAQs

TaxonCMV reportsDistribution of 80 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



## Sequences producing significant alignments:

		(bits)	Value
ref NC_001700_1	Felis catus mitochondrion, complete genome	365	e-101
ref NC_001325_1	Phoca vitulina mitochondrion, complete genome	198	1e-51
ref NC_002008_1	Canis familiaris mitochondrion, complete g...	190	4e-49
ref NC_001602_1	Halichoerus grypus mitochondrion, complete...	180	3e-46
ref NC_000884_1	Cavia porcellus complete mitochondrial genome	176	5e-45
ref NC_001808_1	Ceratotherium simum mitochondrion, complet...	155	2e-41
ref NC_001892_1	Myoxus glis mitochondrion, complete genome	153	8e-38
ref NC_001788_1	Equus asinus mitochondrion, complete genome	151	3e-37
ref NC_002073_1	Orycteropus afer complete mitochondrial ge...	149	1e-36
ref NC_001821_1	Dasyurus novemcinctus mitochondrion, comple...	141	3e-34
ref NC_001779_1	R.unicornis complete mitochondrial genome	135	2e-32
ref NC_001569_1	Mus musculus mitochondrion, complete genome	133	7e-32
ref NC_000889_1	Hippopotamus amphibius mitochondrion, comp...	125	2e-29
ref NC_001640_1	Equus caballus mitochondrion, complete genome	125	2e-29
ref NC_001794_1	Macropus robustus mitochondrion, complete ...	123	7e-29
ref NC_000845_1	Sus scrofa mitochondrion, complete genome	121	3e-28
ref NC_001665_1	Rattus norvegicus mitochondrial genome	121	3e-28
ref NC_001567_1	Bos taurus mitochondrion, complete genome	121	3e-28
ref NC_001643_1	Pan troglodytes mitochondrion, complete ge...	117	4e-27
ref NC_001941_1	Ovis aries mitochondrion, complete genome	109	1e-24
ref NC_002391_1	Talpa europaea mitochondrion, complete genome	103	7e-23
ref NC_001913_1	Oryctolagus cuniculus mitochondrion, compl...	103	7e-23
ref NC_001644_1	Pan paniscus mitochondrion, complete genome	101	3e-22
ref NC_001807_2	Human mitochondrion, complete genome	93	4e-21
ref NC_001601_1	Balaenoptera musculus mitochondrion, compl...	98	4e-21
ref NC_002009_1	Artibeus jamaicensis mitochondrion, comple...	95	2e-20
ref NC_001645_1	Gorilla gorilla mitochondrion, complete ge...	92	2e-19
ref NC_001321_1	Balaenoptera physalus mitochondrion, compl...	90	1e-18
ref NC_001610_1	Didelphis virginiana mitochondrion, comple...	80	9e-16
ref NC_002082_1	Hylobates lar mitochondrion, complete ...	70	9e-13
ref NC_001727_1	Crossostoma lacustre mitochondrion, comple...	70	9e-13
ref NC_001804_1	Latimeria chalumnae mitochondrion, complet...	68	4e-12
ref NC_000880_1	Vidua chalybeata mitochondrion, complete g...	56	1e-11
ref NC_002069_1	Corvus frugilegus mitochondrion, complete ...	54	6e-11
ref NC_000886_1	Chelonia mydas mitochondrial DNA, complete...	52	2e-10
ref NC_001646_1	Pongo pygmaeus mitochondrion, complete genome	52	2e-10
ref NC_001606_1	Cyprinus carpio mitochondrion, complete ge...	50	9e-10
ref NC_000890_1	Mustelus manazo mitochondrion, complete ge...	50	9e-10
ref NC_001323_1	Gallus gallus mitochondrion, complete genome	53	3e-09
ref NC_002079_1	Carassius auratus mitochondrion, complete ...	56	1e-08
ref NC_000934_1	Loxodonta africana mitochondrion, complete...	56	1e-08
ref NC_000878_1	Falco peregrinus mitochondrion, complete g...	56	1e-08
ref NC_000846_1	Rhea americana mitochondrion, complete genome	54	5e-08
ref NC_002196_1	Ictinia boyacana mitochondrion, complete g...	54	5e-08
ref NC_001960_1	Salmo salar mitochondrion, complete genome	54	5e-08
ref NC_001778_1	Polypterus ornatus pinnis mitochondrion, com...	52	2e-07
ref NC_002083_1	Pongo pygmaeus abelii mitochondrion, compl...	52	2e-07
ref NC_001953_1	Struthio camelus complete mitochondrial ge...	52	2e-07
ref NC_001947_1	Pelomedusa subrufa mitochondrion, complete...	52	2e-07
ref NC_001770_1	Acanthocyclops aculeatus mitochondrion, comple...	52	2e-07

## Alignments

tmpseq_0	1	tgaatctgaggaggcttcgttagacaagctaccctgacacgattttgccttccac	60
NC_001700	15524	.....g...g.....C.....d.....g.....	15583
NC_001325	15580	.....a.t.....t.....a..t.a.....C.....	15639
NC_002008	14673	.....C.....G.....a..a.....a.....	14729
NC_001602	15553	.....a.t.....a..t.a..g.....C.....	15612
NC_000884	14650	.....g..g.....C.....a.....	14709
NC_001808	14662	.....a..t.c..t.....C..a..t.....C.....t..	14721
NC_001892	14654	....t....C.....C.....t..a..c.....t..a..t.....	14713
NC_001788	14671	....t..s.....C.....t..C.....t.....	14730
NC_002078	14663	....C.....t.....t.....a..a..a.....C.....	14716
NC_001821	14657	.....a..t..a..c.....C.....	14716
NC_001779	14664	....a..t..a..c.....C.....C..C.....t.....	14723
NC_001662	14625	....t....g.....C.....t..C.....C.....t.....	14684
NC_000882	14658	....t..c.....C.....t.....C.....t.....	14717
NC_001640	14674	....t..s.....C.....t..C.....C.....t.....	14711
NC_001774	14670	....g..s..C.....C.....C..C..C..C.....t.....	14727





<u>NC_000884</u>	14830	..c.....	14846
<u>NC_001808</u>	14842	.....c.....aa..c..c.c.....ac.cgcc..a	14901
<u>NC_001892</u>	14834	..c.....t.....c.a.....a.cc....c..tt.tccc.....acc..a	14893
<u>NC_001788</u>	14851	.....c.....c.....a.a.....	14882
<u>NC_001788</u>	15080	.....	15095
<u>NC_002078</u>	14837	.....	14853
<u>NC_001821</u>	14837	....t.....t.....	14859
<u>NC_001779</u>	14844	.....c.....	14866
<u>NC_001569</u>	14805	.....t.....	14827
<u>NC_000889</u>	14838	..t.....g..c.....	14850
<u>NC_001640</u>	14854	..t..t....t....c.....	14876
<u>NC_001640</u>	15085	.....	15098
<u>NC_001794</u>	14850	..t..t..t.....	14867
<u>NC_000845</u>	16008	.....t..t.....	16024
<u>NC_001665</u>	14790	..t..t.....t.....	14806
<u>NC_001567</u>	15180	....c..c..t..g..c..c.....c.....t.....c..a.....a	15239

\  
ag

<u>NC_001643</u>	14831	.....	14853
<u>NC_001941</u>	14825	..c....c..t....c.....	14847
<u>NC_001913</u>	14841	.....	14857
<u>NC_001544</u>	14832	.....c.....	14854
<u>NC_001807</u>	15413	.....	15429
<u>NC_001601</u>	15276	.....t.....	15292
<u>NC_002009</u>	14816	....t..t..t.....	14835
<u>NC_001645</u>	14835	.....c.....a.....	14863
<u>NC_001321</u>	15279	...c.....t.....	15295
<u>NC_001610</u>	14843	....t..c..a.....	14865
<u>NC_002082</u>	14831	....t.....c.....	14855
<u>NC_001727</u>	15944	....	15947
<u>NC_000880</u>	15652	.....	15659
<u>NC_002069</u>	14364	....t.....	14381
<u>NC_001323</u>	15562	....t.ct.....c..t.....	15588
<u>NC_002079</u>	15962	....	15965
<u>NC_000934</u>	14813	....	14817
<u>NC_000878</u>	14384	....t..tc.....	14406
<u>NC_000846</u>	14307	....	14310
<u>NC_002196</u>	16392	....t..t..cc.....a.....	16421
<u>NC_002083</u>	14867	.....	14895
<u>NC_001953</u>	14290	....	14293

<u>cmpseq_0</u>	241	gtcttattccaccagacctgttaggagaccccgataactatccccggccaaacccttcfa	300
<u>NC_001700</u>	15764	.....t.....c.....a..c.....a.....a.....t..	15823
<u>NC_001325</u>	15820	..g.....c.....a..c.....t.....	15867
<u>NC_002008</u>	14914	....t....t.....a.....a.....c.....a.....c..	14969
<u>NC_001602</u>	15793	..a.....c.....a..g.....c.....t..c..	15852
<u>NC_000884</u>	14900	....c.....a.....a.....ca..c.....g..g	14949
<u>NC_001808</u>	14902	..t.....a.cc.....t..c.....c.....t....	14960
<u>NC_001892</u>	14894	...t.....c.....t.a.....c.....a..c.....a..	14953
<u>NC_002078</u>	14909	.....a.....	14928
<u>NC_000845</u>	16071	.....ac.....a..c.....c..a..a.....a..	16127
<u>NC_001567</u>	15240	..a.....g.....c..cc..c.....a.....c.....c..t	15292
<u>NC_001913</u>	14901	....t.....a.....a..c.....c.....c.....	1492
<u>NC_001644</u>	1484	.....	14962
<u>NC_001807</u>	15476	.....cc..c.....a..c..t..t..c..ta.....cc..	15532
<u>NC_002009</u>	14880	....t.....cc.....a..c..t..t..t..a..a..c..t	14935
<u>NC_001645</u>	14898	.....cc.....a..c.....c..tta.....c..	14954
<u>NC_001510</u>	14907	.....t..t.....c..c..t..c..c..a..t..c..t..	14962
<u>NC_002082</u>	14950	.....	14952
<u>NC_001804</u>	15071	.....a..t..a.....a.....	15108
<u>NC_000985</u>	14980	.....a..c.....c..c..c..a.....	15017
<u>NC_002195</u>	16454	.....ca.....ac.....t.....a..g.....t..c..c..a.....	16507
<u>NC_001950</u>	16155	.....c...	16169

<u>cmpseq_0</u>	301	aatacccccccccataccsaaggctgaaat	128
<u>NC_001700</u>	15824	.....t..a.....	15851
<u>NC_002008</u>	14970	..c.....a..t..a.....	14775
<u>NC_001502</u>	15853	.gc.....a.....	15872
<u>NC_000994</u>	14950	.....	14754
<u>NC_001972</u>	14754	.g.....	14770

63

<u>NC_001772</u>	3081	.....	3094
<u>NC_000845</u>	16128	..c.....a.....	16144
<u>NC_001911</u>	14961	.....	14980
<u>NC_001644</u>	1493	...c.....	1501
<u>NC_001807</u>	15533	..c.....c.....c....	15560
<u>NC_002009</u>	14936	.....c.....a....	14963
<u>NC_001645</u>	14955	.gc.....a.....c.....	14974
<u>NC_001610</u>	14963	..c.....g..c.....a....	14990
<u>NC_002082</u>	14953	..c.....c....	14972
<u>NC_001960</u>	16170	gt...t..a..t.....	16197
<u>NC_001953</u>	14416	.....c....	14437

Database: Sequences from complete mitochondrial genomes

Posted date: Jun 28, 2000 10:56 AM

Number of letters in database: 3,164,247

Number of sequences in database: 129

Lambda      K      H  
1.37      0.711      1.31

Gapped  
Lambda      K      H  
1.37      0.711      1.31

Matrix: blastn matrix:1 -3  
Gap Penalties: Existence: 5, Extension: 2  
Number of Hits to DB: 788  
Number of Sequences: 129  
Number of extensions: 788  
Number of successful extensions: 168  
Number of sequences better than 10.0: 77  
length of query: 328  
length of database: 3,164,247  
effective HSP length: 15  
effective length of query: 313  
effective length of database: 3,162,312  
effective search space: 989803656  
effective search space used: 989803656  
T: 0  
A: 30  
X1: 6 (11.9 bits)  
X2: 15 (29.7 bits)  
S1: 12 (24.3 bits)  
S2: 14 (28.2 bits)

Table 4

BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593400-28182-3122

Query= (328 letters)

Database: nt  
807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Distribution of 50 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



### Sequences producing significant alignments:

			Score (bits)	E Value
Sequences producing significant alignments:				
gb AY005809.1	Panthera pardus cytochrome b gene, partial c...	603	e-170	
gb AF053054.1 AF053054	Panthera tigris sumatrae isolate Sul...	527	e-147	
gb AF053053.1 AF053053	Panthera tigris tigris isolate B7 mi...	527	e-147	
gb AF053050.1 AF053050	Panthera tigris corbetti isolate C2 ...	476	e-132	
gb AF053049.1 AF053049	Panthera tigris corbetti isolate C1 ...	476	e-132	
gb AF053025.1 AF053025	Panthera tigris tigris isolate B9 cy...	450	e-127	
gb AF053024.1 AF053024	Panthera tigris tigris isolate B8 cy...	450	e-127	
gb AF053023.1 AF053023	Panthera tigris tigris isolate B7 cy...	450	e-127	
gb AF053022.1 AF053022	Panthera tigris tigris isolate B6 cy...	450	e-127	
gb AF053021.1 AF053021	Panthera tigris tigris isolate B5 cy...	450	e-127	
gb AF053018.1 AF053018	Panthera tigris tigris isolate B2 cy...	452	e-125	
gb AF053051.1 AF053051	Panthera tigris corbetti isolate C3 ...	452	e-125	
gb AF053048.1 AF053048	Panthera tigris sumatrae isolate Sul...	452	e-125	
gb AF053047.1 AF053047	Panthera tigris sumatrae isolate Su9...	452	e-125	
gb AF053046.1 AF053046	Panthera tigris sumatrae isolate Su7...	452	e-125	
gb AF053045.1 AF053045	Panthera tigris sumatrae isolate Su6...	452	e-125	
gb AF053044.1 AF053044	Panthera tigris sumatrae isolate Su5...	452	e-125	
gb AF053042.1 AF053042	Panthera tigris sumatrae isolate Su3...	452	e-125	
gb AF053041.1 AF053041	Panthera tigris sumatrae isolate Su2...	452	e-125	
gb AF053040.1 AF053040	Panthera tigris sumatrae isolate Sul...	452	e-125	
gb AF053039.1 AF053039	Panthera tigris altaica isolate S15 ...	452	e-125	
gb AF053038.1 AF053038	Panthera tigris altaica isolate S14 ...	452	e-125	
gb AF053037.1 AF053037	Panthera tigris altaica isolate S13 ...	452	e-125	
gb AF053036.1 AF053036	Panthera tigris altaica isolate S12 ...	452	e-125	
gb AF053035.1 AF053035	Panthera tigris altaica isolate S11 ...	452	e-125	
gb AF053034.1 AF053034	Panthera tigris altaica isolate S10 ...	452	e-125	
gb AF053033.1 AF053033	Panthera tigris altaica isolate S8 c...	452	e-125	
gb AF053032.1 AF053032	Panthera tigris altaica isolate S7 c...	452	e-125	
gb AF053031.1 AF053031	Panthera tigris altaica isolate S6 c...	452	e-125	
gb AF053030.1 AF053030	Panthera tigris altaica isolate S5 c...	452	e-125	
gb AF053029.1 AF053029	Panthera tigris altaica isolate S4 c...	452	e-125	
gb AF053028.1 AF053028	Panthera tigris altaica isolate S3 c...	452	e-125	
gb AF053027.1 AF053027	Panthera tigris altaica isolate S2 c...	452	e-125	
gb AF053026.1 AF053026	Panthera tigris tigris isolate B4 cy...	452	e-125	
gb AF053020.1 AF053020	Panthera tigris tigris isolate B3 cy...	452	e-125	
gb AF053019.1 AF053019	Panthera tigris sumatrae isolate Su4...	444	e-122	
gb AF053043.1 AF053043	P.tigris mitochondrial cytochrome b gene	444	e-122	
emb X82301.1 MIPLCYTB	Panthera leo cytochrome b (cytb) gen...	440	e-121	
gb AF053052.1 AF053052	P.l. leo mitochondrial cytochrome b gene	438	e-121	
emb X82300.1 MIPLCYTBG	Felis catus mitochondrial DNA for c...	399	e-106	
gb AB004238.1 AB004238	Felis catus mitochondrial DNA for c...	381	e-103	
gb AB004237.1 AB004237	Felis catus mitochondrial cytochrome...	377	e-102	
emb X82296.1 MIFDCYTB	F.domesticus mitochondrial cytochrome	365	1e-98	
ref NC_001700.1	Felis catus mitochondrion, complete genome	365	1e-98	
gb U20753.1 FCU20753	Felis catus mitochondrion, complete ge...	275	7e-72	
gb AF125145.1 AF125145	Viverricula indica cytochrome b gene...	270	4e-70	
gb AF125144.1 AF125144	Chrotogale owstoni cytochrome b gene...	255	7e-66	
gb AF154975.1 AF154975	Martes martes specimen_voucher AF175...	255	7e-66	
gb AB051237.1 AB051237	Martes martes mitochondrial cytb ge...	255	7e-66	
gb AF125149.1 AF125149	Viverra tangalunga cytochrome b gene...	246	6e-63	

## Alignments

<u>empseq_0</u>	1	cgaatccgaggaggcccctcagtagacauagctaccctgtacacgatccccccgcctttttac	60
<u>AF051059</u>	19	.....g.....c.....	98
<u>AF051054</u>	487	.....g.....c.....	546
<u>AF051051</u>	487	.....g.....c.....	546
<u>AF051050</u>	487	.....g.....c.....	546
<u>AF051049</u>	487	.....g.....c.....	546
<u>AF051025</u>	487	.....g.....c.....	546
<u>AF051024</u>	487	.....g.....c.....	546
<u>AF051032</u>	487	.....g.....c.....	546
<u>AF051033</u>	487	.....g.....c.....	546
<u>AF051031</u>	487	.....g.....c.....	546
<u>AF051019</u>	487	.....g.....c.....	546
<u>AF051051</u>	487	.....g.....c.....	546
<u>AF051042</u>	487	.....g.....c.....	546
<u>AF051047</u>	487	.....g.....c.....	546

<u>AF053046</u>	487	.....g..t.....	546
<u>AF053045</u>	487	.....g..t.....	546
<u>AF053044</u>	487	.....g..t.....	546
<u>AF053042</u>	487	.....g..t.....	546
<u>AF053041</u>	487	.....g..t.....	546
<u>AF053040</u>	487	.....g..t.....	546
<u>AF053039</u>	487	.....g..t.....	546
<u>AF053038</u>	487	.....g..t.....	546
<u>AF053037</u>	487	.....g..t.....	546
<u>AF053036</u>	487	.....g..t.....	546
<u>AF053035</u>	487	.....g..t.....	546
<u>AF053034</u>	487	.....g..t.....	546
<u>AF053033</u>	487	.....g..t.....	546
<u>AF053032</u>	487	.....g..t.....	546
<u>AF053031</u>	487	.....g..t.....	546
<u>AF053030</u>	487	.....g..t.....	546
<u>AF053029</u>	487	.....g..t.....	546
<u>AF053028</u>	487	.....g..t.....	546
<u>AF053027</u>	487	.....g..t.....	546
<u>AF053026</u>	487	.....g..t.....	546
<u>AF053020</u>	487	.....g..t.....	546
<u>AF053019</u>	487	.....g..t.....	546
<u>AF053043</u>	487	.....g..t.....	546
<u>X92301</u>	487	.....g..t.....	546
<u>AF053052</u>	487	.....c.....	546
<u>X82300</u>	490	.....c.....	546
<u>A3004238</u>	487	.....c....a.....	546
<u>A3004237</u>	487	.....c....a.....	546
<u>X82295</u>	487	.....c....a.....	546
<u>NC_001700</u>	15524	.....g....g.....	15583
<u>U20753</u>	15524	.....g....g.....	15583
<u>AF125145</u>	357	.....t.....	416
<u>AF125144</u>	357	.....t....g....t....c....a....c.....	416
<u>AF154975</u>	487	.....g....g.....	546
<u>A3051237</u>	487	.....g....g.....	546
<u>AF125149</u>	357	.....g....t.....	416
<u>empseq_0</u>	61	tccatccccatttatccatcgccctagcagcagtccacccctattccatccacgg	120
<u>AY005809</u>	99	.....	158
<u>AF053054</u>	547	.....c.....	606
<u>AF053053</u>	547	.....c.....	606
<u>AF053050</u>	547	.....g.....c.....	606
<u>AF053049</u>	547	.....g.....c.....	606
<u>AF053025</u>	547	.....g....g.....c.....	606
<u>AF053024</u>	547	.....g....g.....c.....	606
<u>AF053023</u>	547	.....g....g.....c.....	606
<u>AF053022</u>	547	.....g....g.....c.....	606
<u>AF053021</u>	547	.....g....g.....c.....	606
<u>AF053018</u>	547	.....g....g.....c.....	606
<u>AF053051</u>	547	.....g....g.....c.....	606
<u>AF053048</u>	547	.....g....g.....c.....	606
<u>AF053047</u>	547	.....g....g.....c.....	606
<u>AF053045</u>	547	.....g....g.....c.....	606
<u>AF053044</u>	547	.....g....g.....c.....	606
<u>AF053042</u>	547	.....g....g.....c.....	606
<u>AF053041</u>	547	.....g....g.....c.....	606
<u>AF053040</u>	547	.....g....g.....c.....	606
<u>AF053039</u>	547	.....g....g.....c.....	606
<u>AF053038</u>	547	.....g....g.....c.....	606
<u>AF053037</u>	547	.....g....g.....c.....	606
<u>AF053036</u>	547	.....g....g.....c.....	606
<u>AF053035</u>	547	.....g....g.....c.....	606
<u>AF053034</u>	547	.....g....g.....c.....	606
<u>AF053033</u>	547	.....g....g.....c.....	606
<u>AF053032</u>	547	.....g....g.....c.....	606
<u>AF053031</u>	547	.....g....g.....c.....	606
<u>AF053030</u>	547	.....g....g.....c.....	606
<u>AF053029</u>	547	.....g....g.....c.....	606
<u>AF053028</u>	547	.....g....g.....c.....	606
<u>AF053027</u>	547	.....g....g.....c.....	606



<u>AY005E09</u>	219	.....c.....	278
<u>AF05J054</u>	667	.....c.....	726
<u>AF05J053</u>	667	.....c.....	726
<u>AF05J050</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J049</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J025</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J024</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J023</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J022</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J021</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J018</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J051</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J048</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J047</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J046</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J045</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J044</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J042</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J041</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J040</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J039</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J038</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J037</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J036</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J035</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J034</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J033</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J032</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J031</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J030</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J029</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J028</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J027</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J026</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J020</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J019</u>	667	.....t.....t.a.....cc.....	726
<u>AF05J043</u>	667	.....t.....t.a.....cc.....	726
X82301	667	.....t.....t.a.....cc.....	726
<u>AF05J052</u>	667	.....t.....a.....	726
X82300	667	.....t.....a.....	726
<u>A8004238</u>	667	.....c.....a.....t.....	726
<u>A8004237</u>	667	.....c.....a.....t.....	726
X82296	667	.....c.....a.....t.....	726
NC_001700	15704	.....c.....a.....t.....	15763
U20751	15704	.....c.....a.....t.....	15763
<u>AF125145</u>	537	.....t.....ac.....a.....c.....t.....c.....	596
<u>AF125144</u>	537	.....t.....c.....gt.....t.....t.....	596
<u>AF154975</u>	667	.....c.....c.....a.....gee.....c.....c.....	726
<u>AB051237</u>	667	.....c.....c.....a.....gee.....t.....c.....	726
<u>AF125149</u>	537	.....t.....t.....a.....t.....c.....c.....	596
empseq_0	241	gccccaccccccaccagacctgttttagggagacccggataactacatccccggccaaaccttcata	300
<u>AY005B09</u>	279	.....t.....c.....	338
<u>AF05J054</u>	727	.....a.....g.....	785
<u>AF05J053</u>	727	.....a.....g.....	785
<u>AF05J050</u>	727	.....a.....c.....	785
<u>AF05J049</u>	727	.....a.....c.....	785
<u>AF05J035</u>	727	.....a.....c.....	785
<u>AF05J034</u>	727	.....a.....c.....	785
<u>AF05J031</u>	727	.....a.....c.....	785
<u>AF05J022</u>	727	.....a.....c.....	785
<u>AF05J021</u>	727	.....a.....c.....	785
<u>AF05J018</u>	727	.....a.....t.....	785
<u>AF05J051</u>	727	.....a.....t.....	785
<u>AF05J049</u>	727	.....a.....t.....	785
<u>AF05J047</u>	727	.....a.....t.....	785
<u>AF05J045</u>	727	.....a.....t.....	785
<u>AF05J042</u>	727	.....a.....t.....	785
<u>AF05J041</u>	727	.....a.....t.....	785

<u>AF053040</u>	727	.....a.....t.....c.....c... 786
<u>AF051039</u>	727	.....a.....t.....c.....c... 786
<u>AF053038</u>	727	.....a.....t.....c.....c... 786
<u>AF051037</u>	727	.....a.....t.....c.....c... 786
<u>AF053036</u>	727	.....a.....t.....c.....c... 786
<u>AF051035</u>	727	.....a.....t.....c.....c... 786
<u>AF051034</u>	727	.....a.....t.....c.....c... 786
<u>AF051033</u>	727	.....a.....t.....c.....c... 786
<u>AF051032</u>	727	.....a.....t.....c.....c... 786
<u>AF053031</u>	727	.....a.....t.....c.....c... 786
<u>AF053030</u>	727	.....a.....t.....c.....c... 785
<u>AF053029</u>	727	.....a.....t.....c.....c... 786
<u>AF051028</u>	727	.....a.....t.....c.....c... 786
<u>AF051027</u>	727	.....a.....t.....c.....c... 786
<u>AF051026</u>	727	.....a.....t.....c.....c... 786
<u>AF053020</u>	727	.....a.....t.....c.....c... 786
<u>AF053019</u>	727	.....a.....t.....c.....c... 786
<u>AF053043</u>	727	.....a.....t.....c.....c... 786
<u>X82301</u>	727	.....a.....t.....c.....c... 786
<u>AF053052</u>	727	.....a.....t.....c.....t.c..c.... 786
<u>X82300</u>	727	.....a.....t.....c.....t.c..c.... 786
<u>A8004238</u>	727	.....c.....a..c.g.....a.....c.. 786
<u>A8004237</u>	727	.....c.....a..c.....a.....c.. 786
<u>X82296</u>	727	.....r..t.....c.....a..c.....a.. 786
<u>NC_001700</u>	15764	.....t.....c.....a..c.....a..t.. 15823
<u>U20753</u>	15764	.....c.....c.....a..c.....a..t.. 15823
<u>AF125145</u>	597	.....t.....t.....a..t.....c..c.... 650
<u>AF125144</u>	597	.....t.....t.....t.....a..c.....c..a.... 656
<u>AF154975</u>	727	.....a.....c.....c.g.....a..c.....c..a..c 786
<u>A8051237</u>	727	.....a.....c.....c.g.....a..c.....c..a..c 786
<u>AF125149</u>	597	.....t.....cc.....a.....c.c..... 656
<u>tmpsec_0</u>	301	aataccccctccccatatatcaagccgtgaat 328
<u>AY005809</u>	339	..... 366
<u>AF053054</u>	787	..c..... 808
<u>AF053053</u>	787	..c..... 808
<u>AF053050</u>	787	.....t.....c.... 814
<u>AF053049</u>	787	.....t.....c.... 814
<u>AF053025</u>	787	.....c.....c.... 814
<u>AF053024</u>	787	.....t.....c.... 814
<u>AF053023</u>	787	.....t.....c.... 814
<u>AF053022</u>	787	.....t.....c.... 814
<u>AF053021</u>	787	.....t.....c.... 814
<u>AF053018</u>	787	.....t.....c.... 814
<u>AF053051</u>	787	.....t.....c.... 814
<u>AF053048</u>	787	.....t.....c.... 814
<u>AF053047</u>	787	.....t.....c.... 814
<u>AF053046</u>	787	.....t.....c.... 814
<u>AF053045</u>	787	.....t.....c.... 814
<u>AF053044</u>	787	.....t.....c.... 814
<u>AF053042</u>	787	.....c.....c.... 814
<u>AF053041</u>	787	.....t.....c.... 814
<u>AF053040</u>	787	.....t.....c.... 814
<u>AF053019</u>	787	.....t.....c.... 814
<u>AF053038</u>	787	.....t.....c.... 814
<u>AF053037</u>	787	.....t.....c.... 814
<u>AF053036</u>	787	.....t.....c.... 814
<u>AF053035</u>	787	.....t.....c.... 814
<u>AF053014</u>	787	.....t.....c.... 814
<u>AF053011</u>	787	.....t.....c.... 814
<u>AF053032</u>	787	.....c.....c.... 814
<u>AF051031</u>	787	.....c.....c.... 814
<u>AF053030</u>	787	.....c.....c.... 814
<u>AF051022</u>	787	.....c.....c.... 814
<u>AF051028</u>	787	.....c.....c.... 814
<u>AF051037</u>	787	.....t.....c.... 814
<u>AF051036</u>	787	.....t.....c.... 814
<u>AF051030</u>	787	.....c.....c.... 814
<u>AF051012</u>	787	.....c.....c.... 814
<u>AF051041</u>	787	.....c.....c.... 814
<u>X82101</u>	787	.....t.....c.... 814

<u>AF051052</u>	787	.gc.....	a.....	812
<u>X92100</u>	787	.gc.....	a.....	814
<u>AB004238</u>	787	.....	c..a.....	814
<u>AB004237</u>	787	.....	c..a.....	814
<u>X82296</u>	787	.....	c..a.....	814
<u>NC_001700</u>	15824	.....	c..a.....	15851
<u>U20753</u>	15824	.....	c..a.....	15851
<u>AF125144</u>	657	..c.....		664
<u>AF154975</u>	787	..c..a..a.....		803
<u>AB051237</u>	787	..c..a..a.....		803
<u>AF125149</u>	657	..c.....		664

Database: nt

Posted date: Mar 2, 2001 12:20 AM

Number of letters in database: 2,863,827,885

Number of sequences in database: 807,597

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3  
 Gap Penalties: Existence: 5, Extension: 2  
 Number of Hits to DB: 460542  
 Number of Sequences: 807597  
 Number of extensions: 460542  
 Number of successful extensions: 22671  
 Number of sequences better than 10.0: 6487  
 length of query: 328  
 length of database: 2,863,827,885  
 effective HSP length: 20  
 effective length of query: 308  
 effective length of database: 2,847,675,945  
 effective search space: 877084191060  
 effective search space used: 877084191060  
 T: 0  
 A: 30  
 X1: 6 (11.9 bits)  
 X2: 15 (29.7 bits)  
 S1: 12 (24.3 bits)  
 S2: 19 (38.2 bits)

**Table 5.** Reference animals and the allocated code numbers included in the study

SN.	Code number	Name of the animal	Zoological name
1	bhz25t	Indian tiger	<i>Panthera tigris tigris</i>
2	bhz26t	Indian tiger	<i>Panthera tigris tigris</i>
3	bhz30t	Indian tiger	<i>Panthera tigris tigris</i>
4	bhz45t	Indian tiger	<i>Panthera tigris tigris</i>
5	bhz56t	Indian tiger	<i>Panthera tigris tigris</i>
6	bhz63t	Indian tiger	<i>Panthera tigris tigris</i>
7	bhz20wt	Indian white tiger	<i>Panthera tigris bengalensis</i>
8	bhz22wt	Indian white tiger	<i>Panthera tigris bengalensis</i>
9	bhz23wt	Indian white tiger	<i>Panthera tigris bengalensis</i>
10	bhz28wt	Indian white tiger	<i>Panthera tigris bengalensis</i>
11	gz1l	Normal leopard	<i>Panthera pardus</i>
12	gz2l	Normal leopard	<i>Panthera pardus</i>
13	gz3l	Normal leopard	<i>Panthera pardus</i>
14	gz21cl	Clouded leopard	<i>Neofelis nebulosa</i>
15	gz22cl	Clouded leopard	<i>Neofelis nebulosa</i>
16	darz14sl	Snow leopard	<i>Panthera unicia</i>
17	darz15sl	Snow leopard	<i>Panthera unicia</i>
18	darz16sl	Snow leopard	<i>Panthera unicia</i>
19	sbz22al	Asiatic lion	<i>Panthera leo persica</i>
20	sbz38al	Asiatic lion	<i>Panthera leo persica</i>
21	sbz39al	Asiatic lion	<i>Panthera leo persica</i>
22	humsk	Human	<i>Homo sapiens sapiens</i>
23	chimss	Chimpanzee	<i>Pan sp.</i>

Table 6. Multiple sequence alignments of the cytochrome b sequences of reference animals with the sequence obtained from confiscated animal remain

sbz22al	TGAATCTGAGGAGCCTTCAGTAGACAAAGCCACCTGACACCGATTCTTGCCTTCCAC	60
sbz38al	TGAATCTGAGGAGCCTTCAGTAGACAAAGCCACCTGACACCGATTCTTGCCTTCCAC	60
sbz39al	TGAATCTGAGGAGCCTTCAGTAGACAAAGCCACCTGACACCGATTCTTGCCTTCCAC	60
adil.flesh	TGAATCTGAGGAGCCTTCAGTAGACAAAGCTACCTTGACACCGATTCTTGCCTTCCAC	60
gz1nl	TGAATCTGAGGAGCCTTCAGTAGACAAAGCTACCTTGACACCGATTCTTGCCTTCCAC	60
gz2nl	TGAATCTGAGGAGCCTTCAGTAGACAAAGCTACCTTGACACCGATTCTTGCCTTCCAC	60
gz3nl	TGAATCTGAGGAGCCTTCAGTAGACAAAGCTACCTTGACACCGATTCTTGCCTTCCAC	60
bhz23wt	TGAATCTGAGGAGGCTTCAGTAGACAAAGCCACCTGACACGGATTCTTGCCTTCCAC	60
bhz28wt	TGAATCTGAGGAGGCTTCAGTAGACAAAGCCACCTGACACGGATTCTTGCCTTCCAC	60
bhz22wt	TGAATCTGAGGAGGCTTCAGTAGACAAAGCCACCTGACACGGATTCTTGCCTTCCAC	60
bhz20wt	TGAATCTGAGGAGGCTTCAGTAGACAAAGCCACCTGACACGGATTCTTGCCTTCCAC	60
bhz63t	TGAATCTGAGGAGGCTTCAGTAGACAAAGCCACCTGACACGGATTCTTGCCTTCCAC	60
bhz56t	TGAATCTGAGGAGGCTTCAGTAGACAAAGCCACCTGACACGGATTCTTGCCTTCCAC	60
bhz26t	TGAATCTGAGGAGGCTTCAGTAGACAAAGCCACCTGACACGGATTCTTGCCTTCCAC	60
bhz30t	TGAATCTGAGGAGGCTTCAGTAGACAAAGCCACCTGACACGGATTCTTGCCTTCCAC	60
bhz45c	TGAATCTGAGGAGGCTTCAGTAGACAAAGCCACCTGACACGGATTCTTGCCTTCCAC	60
bhz25t	TGAATCTGAGGAGGCTTCAGTAGACAAAGCCACCTGACACGGATTCTTGCCTTCCAC	60
dz14s1	TGAATCTGAGGAGGCTTCAGTAGACAAAGCCACCTGACACGGATTCTTGCCTTCCAC	60
dz15s1	TGAATCTGAGGAGGCTTCAGTAGACAAAGCCACCTGACACGGATTCTTGCCTTCCAC	60
dz16s1	TGAATCTGAGGAGGCTTCAGTAGACAAAGCCACCTGACACGGATTCTTGCCTTCCAC	60
gz21cl	TGAATCTGAGGAGGCTTCAGTAGACAAAGCCACCTGACACGGATTCTTGCCTTCCAC	60
gz22cl	TGAATCTGAGGAGGCTACTCAGTAGACAGCCCTAACCTTACACGGATTCTTACCTTCCAC	60
chimss	TGAATCTGAGGAGGCTACTCAGTAGACAGTCCCACCTTACACGGATTCTTACCTTCCAC	60
humsk	TGAATCTGAGGAGGCTACTCAGTAGACAGTCCCACCTTACACGGATTCTTACCTTCCAC	60
*****		
sbz22al	TTCACTCTCCATTATCATCTAGGCCCTAGCAGCAGTCCACCTCCGTTCCTCCATGAA	120
sbz38al	TTCACTCTCCATTATCATCTAGGCCCTAGCAGCAGTCCACCTCCGTTCCTCCATGAA	120
sbz39al	TTCACTCTCCATTATCATCTAGGCCCTAGCAGCAGTCCACCTCCGTTCCTCCATGAA	120
adil.flesh	TTCACTCTCCATTATCATCTAGCTCTAGCAGCAGTCCACCTCCATTCTTCCACGGAG	120
gz1nl	TTCACTCTCCATTATCATCTAGCTCTAGCAGCAGTCCACCTCCATTCTTCCACGGAG	120
gz2nl	TTCACTCTCCATTATCATCTAGCTCTAGCAGCAGTCCACCTCCATTCTTCCACGGAG	120
gz3nl	TTCACTCTCCATTATCATCTAGCTCTAGCAGCAGTCCACCTCCATTCTTCCACGGAG	120
bhz23wt	TTCACTCTCCATTATCATCTAGGCCCTAGCAGCAGTCCACCTCCATTCTTCCATGAG	120
bhz28wt	TTCACTCTCCATTATCATCTAGGCCCTAGCAGCAGTCCACCTCCATTCTTCCATGAG	120
bhz22wt	TTCACTCTCCATTATCATCTAGGCCCTAGCAGCAGTCCACCTCCATTCTTCCATGAG	120
bhz20wt	TTCACTCTCCATTATCATCTAGGCCCTAGCAGCAGTCCACCTCCATTCTTCCATGAG	120
bhz63t	TTCACTCTCCATTATCATCTAGGCCCTAGCAGCAGTCCACCTCCATTCTTCCATGAG	120
bhz56t	TTCACTCTCCATTATCATCTAGGCCCTAGCAGCAGTCCACCTCCATTCTTCCATGAG	120
bhz26t	TTCACTCTCCATTATCATCTAGGCCCTAGCAGCAGTCCACCTCCATTCTTCCATGAG	120
bhz30t	TTCACTCTCCATTATCATCTAGGCCCTAGCAGCAGTCCACCTCCATTCTTCCATGAG	120
bhz45c	TTCACTCTCCATTATCATCTAGGCCCTAGCAGCAGTCCACCTCCATTCTTCCATGAG	120
bhz25t	TTCACTCTCCATTATCATCTAGGCCCTAGCAGCAGTCCACCTCCATTCTTCCATGAG	120
dz14s1	TTCACTCTCCATTATCATCTAGGCCCTAGCAGCAGTCCACCTCCATTCTTCCATGAG	120
dz15s1	TTCACTCTCCATTATCATCTAGGCCCTAGCAGCAGTCCACCTCCATTCTTCCATGAG	120
dz16s1	TTCACTCTCCATTATCATCTAGGCCCTAGCAGCAGTCCACCTCCATTCTTCCATGAG	120
gz21cl	TTCACTCTCCATTATCATCTAGGCCCTAGCAGCAGTCCACCTCCATTCTTCCATGAG	120
gz22cl	TTCACTCTCCATTATCATCTAGGCCCTAGCAGCAGTCCACCTCCATTCTTCCATGAG	120
chimss	TTTATCTTACCCCTTCATTATCACAGGCCCTAACACAGTCCATTCTTACACGGAA	120
humsk	TTCACTCTGCCCTTCATTATCACAGGCCCTAACACAGTCCATTCTTACACGGAA	120
*****		
sbz22al	ACACGGATCTAATAACCCCTCAGGAATGCTACTGACTGAGATAAAAATCCATTCCATGCA	130
sbz39al	ACACGGATCTAATAACCCCTCAGGAATGCTACTGACTGAGATAAAAATCCATTCCATGCA	130

sbz39al	ACAGGATCTAATAACCCCTCAGGAATGGTATCTGACTCAGATAAAATTCCATTCCATCCA	180
adil.flesh	ACAGGATCTAACAAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA	180
gz1nl	ACAGGATCTAACAAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA	180
gz2nl	ACAGGATCTAACAAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCCATTCCACCCA	180
gz3nl	ACAGGATCTAACAAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCCATTCCACCCA	180
bhz23wt	ACAGGATCTAACAAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCCGTTCCACCCA	180
bhz28wt	ACAGGATCTAACAAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCCGTTCCACCCA	180
bhz22wt	ACAGGATCTAACAAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCCGTTCCACCCA	180
bhz20wt	ACAGGATCTAACAAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCCGTTCCACCCA	180
bhz63t	ACAGGATCTAACAAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCCGTTCCACCCA	180
bhz56t	ACAGGATCTAACAAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCCGTTCCACCCA	180
bhz26t	ACAGGATCTAACAAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCCGTTCCACCCA	180
bhz30t	ACAGGATCTAACAAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCCGTTCCACCCA	180
bhz45t	ACAGGATCTAACAAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCCGTTCCACCCA	180
bhz25t	ACAGGATCTAACAAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCCGTTCCACCCA	180
dz14sl	ACAGGATCTAACAAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCCGTTCCACCCA	180
dz15sl	ACAGGATCTAACAAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCCGTTCCACCCA	180
dz16sl	ACAGGATCTAACAAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCCGTTCCACCCA	180
gz21cl	ACAGGATCCAATAACCCCTCAGGAATGGTATCCGATTAGACAAAATTCCGTTCCACCG	180
gz22cl	ACAGGATCCAATAACCCCTCAGGAATGGTATCCGATTAGACAAAATTCCGTTCCACCG	180
chimss	ACAGGATCAAATAACCCCTGGGAATCACCTCCCCTCCGACAAAATTACCTCCACCCC	180
humsk	ACGGGATCAAACAACCCCTAGGAATCACCTCCCATTCCGATAAAATCATCTTCCACCC	180
*****		
sbz22al	TACTATAAACATCAAAGATATCCTAGGCCTCTAGTACTAATCTTAACACTCATACTACTC	240
sbz38al	TACTATAAACATCAAAGATATCCTAGGCCTCTAGTACTAATCTTAACACTCATACTACTC	240
sbz39al	TACTATAAACATCAAAGATATCCTAGGCCTCTAGTACTAATCTTAACACTCATACTACTC	240
adil.flesh	TACTACACAAATCAAAGATATCTGGGCCTCTAGTACTAATCTTAGCACTCATACTACTC	240
gz1nl	TACTACACAAATCAAAGACATCTGGGCCTCTAGTACTAATCTTAGCACTCATACTACTC	240
gz2nl	TACTACACAAATCAAAGACATCTGGGCCTCTAGTACTAATCTTAGCACTCATACTACTC	240
gz3nl	TACTACACAAATCAAAGACATCTGGGCCTCTAGTACTAATCTTAGCACTCATACTACTC	240
bhz23wt	TACTACACAAATCAAAGACATCTGGGCCTCTAGTACTAATCTTAACACTCATACTACTC	240
bhz28wt	TACTACACAAATCAAAGACATCTGGGCCTCTAGTACTAATCTTAACACTCATACTACTC	240
bhz22wt	TACTACACAAATCAAAGACATCTGGGCCTCTAGTACTAATCTTAACACTCATACTACTC	240
bhz20wt	TACTACACAAATCAAAGACATCTGGGCCTCTAGTACTAATCTTAACACTCATACTACTC	240
bhz63t	TACTACACAAATCAAAGACATCTGGGCCTCTAGTACTAATCTTAACACTCATACTACTC	240
bhz56t	TACTACACAAATCAAAGACATCTGGGCCTCTAGTACTAATCTTAACACTCATACTACTC	240
bhz26t	TACTACACAAATCAAAGACATCTGGGCCTCTAGTACTAATCTTAACACTCATACTACTC	240
bhz30t	TACTACACAAATCAAAGACATCTGGGCCTCTAGTACTAATCTTAACACTCATACTACTC	240
bhz45t	TACTACACAAATCAAAGACATCTGGGCCTCTAGTACTAATCTTAACACTCATACTACTC	240
bhz25t	TACTACACAAATCAAAGACATCTGGGCCTCTAGTACTAATCTTAACACTCATACTACTC	240
dz14sl	TACTACACAAATCAAAGACATCTGGGCCTCTAGTACTAATCTTAACACTCATACTACTC	240
dz15sl	TACTACACAAATCAAAGACATCTGGGCCTCTAGTACTAATCTTAACACTCATACTACTC	240
dz16sl	TACTACACAAATCAAAGACATCTGGGCCTCTAGTACTAATCTTAACACTCATACTACTC	240
gz21cl	TACTATAAACATCAAAGATATCTAGGCCTCTAGTCTAAATTCTAGGCCTCACACTACTT	240
gz22cl	TACTATAAACATCAAAGATATCTAGGCCTCTAGTCTAAATTCTAGGCCTCACACTACTT	240
chimss	TACTACACAAATCAAAGACATCTGGGCCTCTAGTCTAAATTCTGGGTATCTTAATGACATTA	240
humsk	TACTACACAAATCAAAGACATCTGGGCCTCTAGTCTAAATTCTGGGTATCTTAATGACATTA	240
*****		
sbz22al	CTCCTATTCTCACCAAGACCTATTAGGAGATCCCCGACAACCTATAACCCCGGCAATCTTCTA	300
sbz38al	CTCCTATTCTCACCAAGACCTATTAGGAGATCCCCGACAACCTATAACCCCGGCAATCTTCTA	300
sbz39al	CTCCTATTCTCACCAAGACCTATTAGGAGATCCCCGACAACCTATAACCCCGGCAATCTTCTA	300
adil.flesh	CTCCTATTCTCACCAAGACCTATTAGGAGATCCCCGACAACCTATAACCCCGGCAATCTTCTA	300
gz1nl	CTCCTATTCTCACCAAGACCTATTAGGAGACCCCCGATAACCTACATCTGGCAACCCCTCTA	300
gz2nl	CTCCTATTCTCACCAAGACCTATTAGGAGACCCCCGATAACCTACATCTGGCAACCCCTCTA	300
gz3nl	CTCCTATTCTCACCAAGACCTATTAGGAGACCCCCGATAACCTACATCCCCGGCAACCCCTCTA	300
bhz23wt	CTCCTATTCTCACCAAGACCTATTAGGAGACCCCCGATAACCTACATCCCCGGCAACCCCTCTA	300

bhz28wt	GTCCTATTCTCACCAAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA	300
bhz22wt	GTCCTATTCTCACCAAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA	300
bhz20wt	GTCCTATTCTCACCAAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA	300
bhz63t	GTCCTATTCTCACCAAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA	300
bhz56t	GTCCTATTCTCACCAAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA	300
bhz26t	GTCCTATTCTCACCAAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA	300
bhz30t	GTCCTATTCTCACCAAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA	300
bhz45t	GTCCTATTCTCACCAAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA	300
bhz25t	GTCCTATTCTCACCAAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA	300
dz14s1	GTCCTATTCTCACCAAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA	300
dz15s1	GTCCTATTCTCACCAAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA	300
dz16s1	GTCCTATTCTCACCAAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA	300
gz21c1	GTTCTATTCTCCCCAGACCTACTAGGAGACCCCTGACAATTACACTCCCCGCCAACCCCTCTA	300
gz22c1	GTTCTATTCTCCCCAGACCTACTAGGAGACCCCTGACAATTACACTCCCCGCCAACCCCTCTA	300
chimss	ACACTATTCTCACCAAGACCTCTGGCGATCCAGACAACCTACCTAGCTAACCCCCCTTA	300
humsk	ACACTATTCTCACCAAGACCTCTAGGCAGACAAATTACCCCTAGCCAACCCCTTA	300
***** * * * * *		
sbz22a1	AGCACCCCTCCCCATATCAAAACCTGAAT	328
sbz38a1	AGCACCCCTCCCCATATCAAAACCTGAAT	328
sbz39a1	AGCACCCCTCCCCATATCAAAACCTGAAT	328
adil.flesh	AATACCCCTCCCCATATCAAGCCTGAAT	328
gz1nl	AATACCCCTCCCCATATCAAGCCTGAAT	328
gz2nl	AATACCCCTCCCCATATCAAGCCTGAAT	328
gz3nl	AATACCCCTCCCCATATCAAGCCTGAAT	328
bhz23wt	AACACCCCTCCCCATATCAAGCGCGAAT	328
bhz28wt	AACACCCCTCCCCATATCAAGCGCGAAT	328
bhz22wt	AACACCCCTCCCCATATCAAGCGCGAAT	328
bhz20wt	AACACCCCTCCCCATATCAAGCGCGAAT	328
bhz63t	AACACCCCTCCCCATATCAAGCGCGAAT	328
bhz56t	AACACCCCTCCCCATATCAAGCGCGAAT	328
bhz26t	AACACCCCTCCCCATATCAAGCGCGAAT	328
bhz30t	AACACCCCTCCCCATATCAAGCGCGAAT	328
bhz45t	AACACCCCTCCCCATATCAAGCGCGAAT	328
bhz25t	AACACCCCTCCCCATATCAAGCGCGAAT	328
dz14s1	AACACCCCTCCCCATATCAAGCGCGAAT	328
dz15s1	AACACCCCTCCCCATATCAAGCGCGAAT	328
dz16s1	AACACCCCTCCCCATATCAAGCGCGAAT	328
gz21c1	AATACCCCTCCCCATATCAAGCCTGAAT	328
gz22c1	AATACCCCTCCCCATATCAAGCCTGAAT	328
chimss	AACACCCCAACCCCACATTAACCCCGAAT	328
humsk	AACACCCCTCCCCACATCAAGCGCGAAT	328
***** * * * * *		

Table 7a

Position	17	25	29	30	31	33	37	39	48	51	52	57	63	67	69	72	75	78	81	82	87	88	91	94	97	99	102	105	108	111	112
adl.msh	T	G	A	A	G	T	C	G	C	T	G	C	C	T	A	T	C	T	T	C	G	G	C	C	C	A	C	C			
gz11	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.		
gz21	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.			
bhz25t	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.			
bhz26t	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.			
bhz30t	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.			
bhz45t	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.			
bhz56t	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.			
bhz20wt	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	C	.	.	.	C	.	.	.	.	.	.	.	.			
bhz22wt	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	C	.	.	.	C	.	.	.	.	.	.	.	.			
bhz23wt	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	C	.	.	.	C	.	.	.	.	.	.	.	.			
dz14wt	.	.	.	.	.	C	T	A	T	C	T	C	T	C	T	C	T	C	T	C	T	C	T	C	T	C	T	C			
dz16wt	.	.	.	.	.	C	T	A	T	C	T	C	T	C	T	C	T	C	T	C	T	C	T	C	T	C	T	C			
sbz22at	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.			
sbz38at	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.			
gz21cl	.	.	.	.	.	C	.	.	.	T	C	.	.	.	C	.	.	C	T	.	T	.	T	.	T	.	T	.			
gz22cl	.	.	.	.	.	C	.	.	T	C	.	.	.	C	.	.	C	T	.	T	.	T	.	T	.	T	.				

Table 7b

Table 7c

Table 7d

Position	273	276	279	282	284	285	287	288	291	294	297	298	302	303	309	315	318	321	323	324
adll.flesh	C	T	C	C	T	C	C	T	C	C	T	C	A	T	T	T	C	G	T	
gz11	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	
gz21	.	.	.	.	.	.	.	C.	.	.	.	.	.	.	.	.	.	.	.	
gz22	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.	.	.	.	
bhz25t	.	.	.	.	.	.	C	.	.	.	.	C	.	.	.	.	G	C		
bhz26t	.	.	.	.	.	.	C	.	.	.	C	.	.	.	.	G	C			
bhz30t	.	.	.	.	.	C	.	.	.	C	.	.	.	.	G	C				
bhz45t	.	.	.	.	C	.	.	.	C	.	C	.	.	.	G	C				
bhz56t	.	.	.	C	.	.	C	.	C	.	C	.	.	.	G	C				
bhz20wt	.	.	C	.	C	.	C	.	C	.	C	.	C	.	G	C				
bhz22wt	.	.	C	.	C	.	C	.	C	.	C	.	C	.	G	C				
bhz23wt	.	.	C	.	C	.	C	.	C	.	C	.	C	.	G	C				
dz14sl	.	.	C	.	C	.	C	.	C	.	C	.	C	.	C	.	C			
dz15sl	.	.	C	.	C	.	C	.	C	.	C	.	C	.	C	.	C			
sbz22al	.	C	T	C	.	C	T	.	G	C	.	A	.	.	.	.	.	.		
sbz38al	.	C	T	C	.	C	T	.	G	C	.	A	.	.	.	.	.	.		
gz21cl	T	C	T	C	T	C	.	.	.	.	.	.	.	.	.	.	.	.		
gz22cl	T	C	T	C	T	C	.	.	.	.	.	.	.	.	.	.	.	.		
chimss	T	A	T	C	T	A	T	C	T	A	T	C	T	A	T	C	T	A		
humsk	T	A	T	C	T	A	T	C	T	A	T	C	T	A	T	C	T	A		

Table 8. Percent similarity matrix calculated by pair-wise comparisons of cytochrome b gene sequences revealed from 'adil.flesh' and different felids

	bhz20wt	bhz25t	dz14sl	humsk	chlms	sbz22al	gz1L	gz2L	gz3L	gz21cl	adil.flesh
bhz20wt	[REDACTED]	100	99.1	81.7	78.7	93.3	95.1	95.4	95.4	89.6	95.4
bhz25t	100	[REDACTED]	99.1	81.7	78.7	93.3	95.1	95.4	95.4	89.6	95.4
dz14sl	99.1	99.1	[REDACTED]	81.4	78.4	93	94.8	95.1	95.1	89.3	95.1
humsk	81.7	81.7	81.4	[REDACTED]	86.9	79.6	81.1	80.2	80.2	79	81.4
chlms	78.7	78.7	78.4	86.9	[REDACTED]	78.7	79.6	78.7	78.7	76.8	79.9
sbz22al	93.3	93.3	93	79.6	78.7	[REDACTED]	92.1	92.4	92.4	89	92.4
gz1L	95.1	95.1	94.8	81.1	79.6	92.1	[REDACTED]	98.5	98.5	89.3	99.7
gz2L	95.4	95.4	95.1	80.2	78.7	92.4	98.5	[REDACTED]	100	88.1	98.2
gz3L	95.4	95.4	95.1	80.2	78.7	92.4	98.5	100	[REDACTED]	88.1	98.2
gz21cl	89.6	89.6	89.3	79	76.8	89	89.3	88.1	[REDACTED]	89.6	
adil.flesh	95.4	95.4	95.1	81.4	79.9	92.4	99.7	98.2	98.2	89.6	

## Table 1C



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984591695-10075-13605

Query=

(25 letters)

Database: nt

807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reportsDistribution of 500 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



## Sequences producing significant alignments:

			Score (bits)	E Value
gb AF231651.1 AF231651	Strongylura notata clone HB-82 cytoc...	50	2e-05	
gb AF231650.1 AF231650	Strongylura notata clone HB-159 cyto...	50	2e-05	
ref NC_002672.1	Dinornis giganteus mitochondrion, complete...	50	2e-05	
ref NC_002673.1	Emeus crassus mitochondrion, complete genome	50	2e-05	
gb AF232015.1 AF232015	Nothrotheriops shastensis cytochrome...	50	2e-05	
gb AF232013.1 AF232013	Bradypus variegatus cytochrome b gene...	50	2e-05	
gb AY016015.1	Emeus crassus mitochondrion, complete genome	50	2e-05	
gb AY016013.1	Dinornis giganteus mitochondrion, complete genome	50	2e-05	
gb AY016014.1	Dromaius novaehollandiae mitochondrion, part...	50	2e-05	
gb AF230167.1 AF230167	Bonasa umbellus cytochrome b (CYTB) ...	50	2e-05	
gb AF074594.1 AF074594	Baeolophus bicolor cytochrome b gene...	50	2e-05	
gb AY005210.1	Poospiza melanoleuca isolate 3 cytochrome b ...	50	2e-05	
gb AY005209.1	Poospiza melanoleuca isolate 2 cytochrome b ...	50	2e-05	
gb AY005208.1	Poospiza melanoleuca isolate 1 cytochrome b ...	50	2e-05	
gb AY005205.1	Poospiza hispaniolensis cytochrome b (cytb) ...	50	2e-05	
gb AY005204.1	Poospiza garleppi cytochrome b (cytb) gene, ...	50	2e-05	
gb AY005203.1	Poospiza erythroryncha cytochrome b (cytb) ge...	50	2e-05	
gb AY005201.1	Poospiza boliviana cytochrome b (cytb) gene, ...	50	2e-05	
gb AY005199.1	Poospiza alticola isolate 2 cytochrome b (cy...)	50	2e-05	
gb AY005198.1	Poospiza alticola isolate 1 cytochrome b (cy...)	50	2e-05	
cb AF155870.1 AF155870	Heterocephalus glaber cytochrome b (...)	50	2e-05	
gb AF189123.1 AF189123	Glyptotermes eukalypti cytochrome b ...	50	2e-05	
gb AF102099.1 AF102099	Criniferoides leucogaster cytochrome...	50	2e-05	
gb AF102095.1 AF102095S1	Corythaixoides concolor cytochrome...	50	2e-05	
cb AF271065.1 AF271065	Mustela erminea specimen-voucher AF1...	50	2e-05	
gb AF243857.1 AF243857	Strongylura notata notata cytochrome...	50	2e-05	
cb AF243856.1 AF243856	Strongylura notata forsychia cytochr...	50	2e-05	
ref NC_001567.1	Bos taurus mitochondrion, complete genome	50	2e-05	
cb AF306872.1 AF306872	Brachyramphus marmoratus haplotype M...	50	2e-05	
cb AF306871.1 AF306871	Brachyramphus marmoratus haplotype M...	50	2e-05	
gb AF306870.1 AF306870	Brachyramphus brevirostris haplotype...	50	2e-05	
cb AF306869.1 AF306869	Brachyramphus brevirostris haplotype...	50	2e-05	
gb AF306868.1 AF306868	Brachyramphus brevirostris haplotype...	50	2e-05	
gb AF010406.1 AF010406	Ovis aries complete mitochondrial ge...	50	2e-05	
cb AF248662.1 AF248662	Gryllus campestris haplotype 2 cytoc...	50	2e-05	
cb AF248661.1 AF248661	Gryllus campestris haplotype 1 cytoc...	50	2e-05	
cb AF096462.1 AF096462	Rhipidura albicollis cytochrome b ge...	50	2e-05	
gb AF283644.1 AF283644	Elaphe obsoleta cytochrome b gene, c...	50	2e-05	
gb AF283643.1 AF283643	Elaphe obsoleta cytochrome b gene, c...	50	2e-05	
gb AF283642.1 AF283642	Elaphe obsoleta cytochrome b gene, c...	50	2e-05	
gb AF283641.1 AF283641	Elaphe obsoleta cytochrome b gene, c...	50	2e-05	
gb AF283640.1 AF283640	Elaphe obsoleta cytochrome b gene, c...	50	2e-05	
gb AF283639.1 AF283639	Elaphe obsoleta cytochrome b gene, c...	50	2e-05	
gb AF283637.1 AF283637	Elaphe obsoleta LSUMZ 45359 cytochro...	50	2e-05	
gb AF283636.1 AF283636	Elaphe obsoleta LSUMZ 44662 cytochro...	50	2e-05	
gb AF283635.1 AF283635	Elaphe obsoleta LSUMZ 40443 cytochro...	50	2e-05	
gb AF283634.1 AF283634	Elaphe obsoleta LSUMZ 44335 cytochro...	50	2e-05	
gb AF283633.1 AF283633	Elaphe obsoleta LSUMZ 42624 cytochro...	50	2e-05	
gb AF283632.1 AF283632	Elaphe obsoleta LSUMZ H1911 cytochro...	50	2e-05	
gb AF283631.1 AF283631	Elaphe obsoleta LSUMZ 41197 cytochro...	50	2e-05	
gb AF283630.1 AF283630	Elaphe obsoleta LSUMZ 41189 cytochro...	50	2e-05	
gb AF283629.1 AF283629	Elaphe obsoleta LSUMZ 41188 cytochro...	50	2e-05	
gb AF283628.1 AF283628	Elaphe obsoleta LSUMZ 41187 cytochro...	50	2e-05	
gb AF283627.1 AF283627	Elaphe obsoleta LSUMZ 41186 cytochro...	50	2e-05	
gb AF283626.1 AF283626	Elaphe obsoleta LSUMZ 40943 cytochro...	50	2e-05	
gb AF283625.1 AF283625	Elaphe obsoleta LSUMZ 37499 cytochro...	50	2e-05	
gb AF283624.1 AF283624	Elaphe obsoleta LSUMZ 44480 cytochro...	50	2e-05	
gb AF283623.1 AF283623	Elaphe obsoleta LSUMZ 44451 cytochro...	50	2e-05	
gb AF283622.1 AF283622	Elaphe obsoleta LSUMZ 40444 cytochro...	50	2e-05	
gb AF283621.1 AF283621	Elaphe obsoleta LSUMZ 39925 cytochro...	50	2e-05	
gb AF283620.1 AF283620	Elaphe obsoleta LSUMZ 39163 cytochro...	50	2e-05	
gb AF283619.1 AF283619	Elaphe obsoleta LSUMZ 39162 cytochro...	50	2e-05	
gb AF283618.1 AF283618	Elaphe obsoleta LSUMZ H15876 cytochro...	50	2e-05	
gb AF283617.1 AF283617	Elaphe obsoleta LSUMZ H15872 cytochro...	50	2e-05	
gb AF283616.1 AF283616	Elaphe obsoleta LSUMZ 15871 cytochro...	50	2e-05	
gb AF283615.1 AF283615	Elaphe obsoleta LSUMZ H15870 cytochro...	50	2e-05	
gb AF283614.1 AF283614	Elaphe obsoleta LSUMZ H15867 cytochro...	50	2e-05	
gb AF283613.1 AF283613	Elaphe obsoleta LSUMZ H15864 cytochro...	50	2e-05	

**Table 9.** Animals selected for validation of minimum P'S score for efficient amplification of DNA templates in PCR

SL.	Name	P, S/AFF	P, S/AFR
1	Indian black buck ( <i>Antilope cervicapra</i> )	97, 58	96, 54
2	Sheep ( <i>Ovis</i>	87, 53	96, 54
3	Pig ( <i>Sus scrofa</i> )	87, 52	87, 41
4	Fresh water dolphin ( <i>Platanista gangetica</i> )	86, 49	82, 47

## Sequences producing significant alignments:

		Score (bits)	E Value
gb AF231651_1 AF231651	Strongylura notata clone HB-82 cytoc...	50	2e-05
gb AF231650_1 AF231650	Strongylura notata clone HB-159 cyto...	50	2e-05
ref NC_002672_1	Dinornis giganteus mitochondrion, complete...	50	2e-05
ref NC_002673_1	Emeus crassus mitochondrion, complete genome	50	2e-05
gb AF232015_1 AF232015	Nothrotheriops shastensis cytochrome...	50	2e-05
gb AF232013_1 AF232013	Bradypus variegatus cytochrome b gen...	50	2e-05
gb AY016015_1	Emeus crassus mitochondrion, complete genome	50	2e-05
gb AY016013_1	Dinornis giganteus mitochondrion, complete g...	50	2e-05
gb AY016014_1	Dromaius novaehollandiae mitochondrion, part...	50	2e-05
gb AF230167_1 AF230167	Bonasa umbellus cytochrome b (CYTB) ...	50	2e-05
gb AF074594_1 AF074594	Baeolophus bicolor cytochrome b gene...	50	2e-05
gb AY005210_1	Poospiza melanoleuca isolate 3 cytochrome b ...	50	2e-05
gb AY005209_1	Poospiza melanoleuca isolate 2 cytochrome b ...	50	2e-05
gb AY005208_1	Poospiza melanoleuca isolate 1 cytochrome b ...	50	2e-05
gb AY005205_1	Poospiza hispaniolensis cytochrome b (cytb) ...	50	2e-05
gb AY005204_1	Poospiza garleppi cytochrome b (cytb) gene, ...	50	2e-05
gb AY005203_1	Poospiza erythrophrys cytochrome b (cytb) ge...	50	2e-05
gb AY005201_1	Poospiza boliviana cytochrome b (cytb) gene,...	50	2e-05
gb AY005199_1	Poospiza alticola isolate 2 cytochrome b (cy...	50	2e-05
gb AY005198_1	Poospiza alticola isolate 1 cytochrome b (cy...	50	2e-05
gb AF155870_1 AF155870	Heterocephalus glaber cytochrome b (...)	50	2e-05
gb AF189123_1 AF189123	Glyptotermes eukalypti cytochrome b ...	50	2e-05
gb AF102099_1 AF102099	Criniferoides leucogaster cytochrome...	50	2e-05
gb AF102095_1 AF102095S1	Corythaixoides concolor cytochrome...	50	2e-05
gb AF271065_1 AF271065	Mustela erminea specimen-voucher Af1...	50	2e-05
gb AF243857_1 AF243857	Strongylura notata notata cytochrome...	50	2e-05
gb AF243856_1 AF243856	Strongylura notata forsythia cytochr...	50	2e-05
ref NC_001567_1	Bos taurus mitochondrion, complete genome	50	2e-05
gb AF306872_1 AF306872	Brachyramphus marmoratus haplotype M...	50	2e-05
gb AF306871_1 AF306871	Brachyramphus marmoratus haplotype M...	50	2e-05
gb AF306870_1 AF306870	Brachyramphus brevirostris haplotype...	50	2e-05
gb AF306869_1 AF306869	Brachyramphus brevirostris haplotype...	50	2e-05
gb AF306868_1 AF306868	Brachyramphus brevirostris haplotype...	50	2e-05
gb AF010406_1 AF010406	Ovis aries complete mitochondrial ge...	50	2e-05
gb AF248662_1 AF248662	Gryllus campestris haplotype 2 cytoc...	50	2e-05
gb AF248661_1 AF248661	Gryllus campestris haplotype 1 cytoc...	50	2e-05
gb AF096462_1 AF096462	Rhipidura albicollis cytochrome b ge...	50	2e-05
gb AF283644_1 AF283644	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283643_1 AF283643	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283642_1 AF283642	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283641_1 AF283641	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283640_1 AF283640	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283639_1 AF283639	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283637_1 AF283637	Elaphe obsoleta LSUMZ 45359 cytochro...	50	2e-05
gb AF283636_1 AF283636	Elaphe obsoleta LSUMZ 44662 cytochro...	50	2e-05
gb AF283635_1 AF283635	Elaphe obsoleta LSUMZ 40443 cytochro...	50	2e-05
gb AF283634_1 AF283634	Elaphe obsoleta LSUMZ 44335 cytochro...	50	2e-05
gb AF283633_1 AF283633	Elaphe obsoleta LSUMZ 42624 cytochro...	50	2e-05
gb AF283632_1 AF283632	Elaphe obsoleta LSUMZ H1911 cytochro...	50	2e-05
gb AF283631_1 AF283631	Elaphe obsoleta LSUMZ 41197 cytochro...	50	2e-05
gb AF283630_1 AF283630	Elaphe obsoleta LSUMZ 41189 cytochro...	50	2e-05
gb AF283629_1 AF283629	Elaphe obsoleta LSUMZ 41188 cytochro...	50	2e-05
gb AF283628_1 AF283628	Elaphe obsoleta LSUMZ 41187 cytochro...	50	2e-05
gb AF283627_1 AF283627	Elaphe obsoleta LSUMZ 41186 cytochro...	50	2e-05
gb AF283626_1 AF283626	Elaphe obsoleta LSUMZ 40943 cytochro...	50	2e-05
gb AF283625_1 AF283625	Elaphe obsoleta LSUMZ 37499 cytochro...	50	2e-05
gb AF283624_1 AF283624	Elaphe obsoleta LSUMZ 44480 cytochro...	50	2e-05
gb AF283623_1 AF283623	Elaphe obsoleta LSUMZ 44451 cytochro...	50	2e-05
gb AF283622_1 AF283622	Elaphe obsoleta LSUMZ 40444 cytochro...	50	2e-05
gb AF283621_1 AF283621	Elaphe obsoleta LSUMZ 39925 cytochro...	50	2e-05
gb AF283620_1 AF283620	Elaphe obsoleta LSUMZ 39163 cytochro...	50	2e-05
gb AF283619_1 AF283619	Elaphe obsoleta LSUMZ 39162 cytochrom...	50	2e-05
gb AF283618_1 AF283618	Elaphe obsoleta LSUMZ H19896 cytochr...	50	2e-05
gb AF283617_1 AF283617	Elaphe obsoleta LSUMZ H19832 cytochr...	50	2e-05
gb AF283616_1 AF283616	Elaphe obsoleta LSUMZ 15891 cytochro...	50	2e-05
gb AF283615_1 AF283615	Elaphe obsoleta LSUMZ H19890 cytochr...	50	2e-05
gb AF283614_1 AF283614	Elaphe obsoleta LSUMZ H19889 cytochr...	50	2e-05
gb AF283613_1 AF283613	Elaphe obsoleta LSUMZ H19888 cytochr...	50	2e-05

gb AF283612..1 AF283612	Elaphe obsoleta LSUMZ H15884 cytochr...	50	2e-05
gb AF283611..1 AF283611	Elaphe obsoleta LSUMZ H15031 cytochr...	50	2e-05
gb AF283610..1 AF283610	Elaphe obsoleta LSUMZ H15030 cytochr...	50	2e-05
gb AF283609..1 AF283609	Elaphe obsoleta CAS 169468 cytochrom...	50	2e-05
gb AF283608..1 AF283608	Elaphe obsoleta LSUMZ H14781 cytochr...	50	2e-05
gb AF283607..1 AF283607	Elaphe obsoleta LSUMZ H14724 cytochr...	50	2e-05
gb AF283606..1 AF283606	Elaphe obsoleta cytochrome b gene. c...	50	2e-05
gb AF283605..1 AF283605	Elaphe obsoleta cytochrome b gene. c...	50	2e-05
gb AF283604..1 AF283604	Elaphe obsoleta cytochrome b gene. c...	50	2e-05
gb AF283603..1 AF283603	Elaphe obsoleta LSUMZ H3388 cytochro...	50	2e-05
gb AF283602..1 AF283602	Elaphe obsoleta LSUMZ H3385 cytochro...	50	2e-05
gb AF283601..1 AF283601	Elaphe obsoleta LSUMZ H3384 cytochro...	50	2e-05
gb AF283600..1 AF283600	Elaphe obsoleta LSUMZ H3382 cytochrome...	50	2e-05
gb AF283599..1 AF283599	Elaphe bairdi LSUMZ H3381 cytochrome...	50	2e-05
gb AF283598..1 AF283598	Elaphe obsoleta LSUMZ H3379 cytochro...	50	2e-05
gb AF283597..1 AF283597	Elaphe obsoleta LSUMZ 39616 cytochro...	50	2e-05
gb AF283596..1 AF283596	Elaphe obsoleta LSUMZ H3376 cytochro...	50	2e-05
gb AF283595..1 AF283595	Elaphe obsoleta LSUMZ H3345 cytochro...	50	2e-05
gb AF283594..1 AF283594	Elaphe obsoleta LSUMZ H3309 cytochro...	50	2e-05
gb AF283593..1 AF283593	Elaphe obsoleta LSUMZ H3306 cytochro...	50	2e-05
gb AF283592..1 AF283592	Elaphe obsoleta LSUMZ H3276 cytochro...	50	2e-05
gb AF283591..1 AF283591	Elaphe obsoleta LSUMZ H3246 cytochro...	50	2e-05
gb AF283590..1 AF283590	Elaphe obsoleta LSUMZ H3212 cytochro...	50	2e-05
gb AF283589..1 AF283589	Elaphe obsoleta LSUMZ H3209 cytochro...	50	2e-05
gb AF283588..1 AF283588	Elaphe obsoleta LSUMZ H3206 cytochro...	50	2e-05
gb AF283587..1 AF283587	Elaphe obsoleta LSUMZ H3191 cytochro...	50	2e-05
gb AF283586..1 AF283586	Elaphe obsoleta LSUMZ H3190 cytochro...	50	2e-05
gb AF283585..1 AF283585	Elaphe obsoleta LSUMZ H3189 cytochro...	50	2e-05
gb AF283584..1 AF283584	Elaphe obsoleta LSUMZ H3188 cytochro...	50	2e-05
gb AF283583..1 AF283583	Elaphe obsoleta LSUMZ H3186 cytochro...	50	2e-05
gb AF283582..1 AF283582	Elaphe obsoleta LSUMZ H3169 cytochro...	50	2e-05
gb AF283581..1 AF283581	Elaphe obsoleta LSUMZ CAS 203083 cytochrom...	50	2e-05
gb AF283580..1 AF283580	Elaphe obsoleta LSUMZ CAS 203079 cytochrom...	50	2e-05
gb AF283579..1 AF283579	Elaphe obsoleta LSUMZ H2286 cytochro...	50	2e-05
gb AF283578..1 AF283578	Elaphe obsoleta CAS 208631 cytochrom...	50	2e-05
gb AF283577..1 AF283577	Elaphe obsoleta LSUMZ H2229 cytochro...	50	2e-05
gb AF283576..1 AF283576	Rhinophylla pumilio isolate TK46001 ...	50	2e-05
gb AF187030..1 AF187030	Poospiza hispaniolensis cytochrome b...	50	2e-05
gb AF310052..1 AF310052	Valatinia jacarina cytochrome b gene...	50	2e-05
gb AF310046..1 AF310046	Deinagkistrodon acutus cytochrome b ...	50	2e-05
gb AF171919..1 AF171919	Trimeresurus mucrosquamatus cyt b gen...	50	2e-05
gb AF171897..1 AF171897	Agelaius cyanopus cytochrome b (cytb...)	50	2e-05
gb AF290174..1 AF290174	Agelaius phoeniceus cytochrome b (cy...	50	2e-05
gb AF290173..1 AF290173	Quiscalus major cytochrome b (cytb) ...	50	2e-05
gb AF290171..1 AF290171	Amblycercus holosericeus cytochrome ...	50	2e-05
gb AF290170..1 AF290170	Volatinia jacarina cytochrome b (cyt...)	50	2e-05
gb AF290150..1 AF290150	Reithrodontomys zacatecae cytochrome...	50	2e-05
gb AF176252..1 AF176252	Reithrodontomys zacatecae cytochrome...	50	2e-05
gb AF176251..1 AF176251	Microtus xanthognathus cytochrome b ...	50	2e-05
gb AF163907..1 AF163907	Microtus pinetorum cytochrome b gene...	50	2e-05
gb AF163904..1 AF163904	Microtus ochrogaster cytochrome b ge...	50	2e-05
gb AF163901..1 AF163901	Microtus mizuris cytochrome b gene. c...	50	2e-05
gb AF163899..1 AF163899	Microtus californicus cytochrome B (...)	50	2e-05
gb AF163891..1 AF163891	Microtus abbreviatus cytochrome B (c...	50	2e-05
gb AF163890..1 AF163890	Dipsoschelys dussumieri isolate Germa...	50	2e-05
gb AF288521..1 AF288524	Dipsoschelys dussumieri isolate white...	50	2e-05
gb AF288523..1 AF288523	Dipsoschelys dussumieri isolate Aldy ...	50	2e-05
gb AF288522..1 AF288522	Psilopogon pyrolophus cytochrome b (...)	50	2e-05
gb AF123510..1 AF123510	Eubucco bourcierii cucinkae cytochro...	50	2e-05
gb AF123512..1 AF123512	Adolfus vauesezeelli cytochrome b gen...	50	2e-05
gb AF206548..1 AF206548	Gymnochima tibicen cytochrome b gene...	50	2e-05
gb AF197857..1 AF197857	Sitta europaea cytochrome b gene, part...	50	2e-05
gb U61197..3 SEU61197	Dinodon semicarinatus mitochondrion, compl...	50	2e-05
gb INC 001945..1 INC 001945	Oasypus novemcinctus mitochondrion, comple...	50	2e-05
gb INC 001851..1 INC 001851	Daeymyia incomta country Tanzania cy...	50	2e-05
gb AF141217..1 AF141217	Pantodon buchholzi cytochrome b gene...	50	2e-05
gb AF201615..1 AF201615	Bombus nevadensis cytochrome b gene....	50	2e-05
gb AF077930..1 AF077930	Oreamnos americanus cytochrome b (cy...	50	2e-05
gb AF190612..1 AF190612	taurus mitochondrion, complete genome	50	2e-05
gb J01129..1 BQVMT_808	Cochlearius cochlearius cytochrome b...	50	2e-05
gb AF191810..1 AF191810		50	2e-05

gb U89181.1 CAU89181	Chlorostilbon aureonotatus cytochrome ...	50	2e-05
gb U89171.1 AFU89171	Asia flammeus cytochrome b (cytb) gene...	50	2e-05
gb AF217833.1 AF217833	Hemoroselaps lacteus cytochrome b ge...	50	2e-05
gb AF217822.1 AF217822	Hydrophis semperi cytochrome b gene, ...	50	2e-05
gb AF217813.1 AF217813	Acanthophis antarcticus cytochrome b...	50	2e-05
gb AF220406.1 AF220406	Calliophis kelloggi cytochrome b (cy...)	50	2e-05
gb AF126430.1 AF126430	Ellobius fuscocapillus cytochrome b ...	50	2e-05
gb AF090337.1 AF090337	Aythya americana mitochondrion, comp...	50	2e-05
gb AF059111.1 AF059111	Sackidiornis melanotos cytochrome b ...	50	2e-05
gb AF059053.1 AF059053	Aix sponsa cytochrome b gene, partial...	50	2e-05
gb AF099308.1 AF099308	Icterus wagleri wagleri cytochrome b...	50	2e-05
gb AF099295.1 AF099295	Icterus gularis yucatanensis cytochr...	50	2e-05
gb AF099294.1 AF099294	Icterus gularis tamaulipensis cytoch...	50	2e-05
gb AF099293.1 AF099293	Icterus gularis gularis cytochrome b...	50	2e-05
gb AF160610.1 AF160610	Cricetomys emini Cemi636 cytochrome ...	50	2e-05
gb AF036280.1 AF036280	Tragelaphus strepsiceros cytochrome ...	50	2e-05
gb AF036277.1 AF036277	Tragelaphus scriptus cytochrome b (cy...)	50	2e-05
gb AF036274.1	Tetracerus quadricornis cytochrome b (cytb) ...	50	2e-05
gb AF194218.1 AF194218	Phrynosoma platyrhinos cytochrome b ...	50	2e-05
gb AF194216.1 AF194216	Urosaurus ornatus cytochrome b gene, ...	50	2e-05
ref NC_002009.1	Artibeus jamaicensis mitochondrion, comple...	50	2e-05
ref NC_001941.1	Ovis aries mitochondrion, complete genome	50	2e-05
ref NC_000877.1	Aythya americana mitochondrion, complete g...	50	2e-05
ref NC_000846.1	Rhea americana mitochondrion, complete genome	50	2e-05
gb U27551.1 GCU27551	Grus canadensis tabida cytochrome b (c...	50	2e-05
gb AF089058.1 AF089058	Quiscalus quiscula cytochrome b (cyt...)	50	2e-05
gb AF089055.1 AF089055	Quiscalus major cytochrome b (cytb) ...	50	2e-05
gb AF089054.1 AF089054	Quiscalus lugubris cytochrome b (cyt...)	50	2e-05
gb AF089046.1 AF089046	Oreopsar bolivianus cytochrome b (cy...)	50	2e-05
gb AF089042.1 AF089042	Molothrus badius cytochrome b (cytb) ...	50	2e-05
gb AF089039.1 AF089039	Macroagelaius imthurni cytochrome b ...	50	2e-05
gb AF089037.1 AF089037	Lampropsartanagrinus cytochrome b (...)	50	2e-05
gb AF089026.1 AF089026	Gymnomystax mexicanus cytochrome b (...)	50	2e-05
gb AF089025.1 AF089025	Gnorimopsar chopi cytochrome b (cytb...)	50	2e-05
gb AF089024.1 AF089024	Euphagus cyanocephalus cytochrome b ...	50	2e-05
gb AF089023.1 AF089023	Euphagus carolinus cytochrome b (cyt...)	50	2e-05
gb AF089021.1 AF089021	Dives warzewitschi cytochrome b (cyt...)	50	2e-05
gb AF089020.1 AF089020	Curaeus curaeus cytochrome b (cytb) ...	50	2e-05
gb AF089016.1 AF089016	Amblycercus holosericeus cytochrome ...	50	2e-05
gb AF089013.1 AF089013	Agelaius xanthophthalmus cytochrome ...	50	2e-05
gb AF089012.1 AF089012	Agelaius xanthomus cytochrome b (cyt...)	50	2e-05
gb AF089008.1 AF089008	Agelaius phoeniceus sub-species phoe...	50	2e-05
gb AF089006.1 AF089006	. Agelaius humeralis cytochrome b (cyt...)	50	2e-05
gb AF089005.1 AF089005	Agelaius cyanopus cytochrome b (cytb...)	50	2e-05
gb AF108695.1 AF108695	Scolomys juruaense cytochrome B (cyt...)	50	2e-05
gb AF108685.1 AF108685	Wiedomys pyrrhorhinos cytochrome B (...)	50	2e-05
gb AF108677.1 AF108677	Thomasomys oreas cytochrome B (cytB) ...	50	2e-05
gb AF145511.1 AF145511	Melanoplus foedus cytochrome b gene, ...	50	2e-05
gb AF145511.1 AF145511	Melanoplus angustipennis cytochrome ...	50	2e-05
gb U89627.1 BMU89627	Bolitoglossa marmorea cytochrome b (cy...)	50	2e-05
gb U89623.1 BPU89623	Batrachoseps pacificus cytochrome b (c...	50	2e-05
gb AF181470.1 AF181470	Okapia johnstoni cytochrome b gene, ...	50	2e-05
gb AF094075.1 AF094075	Lagenostomus acutus cytochrome b g...	50	2e-05
gb U90303.1 OMU90303	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb U90302.1 OMU90302	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb U90301.1 OMU90301	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb U90300.1 OMU90300	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb AF038883.1 AF038883	Deinagkistrodon acutus cytochrome b ...	50	2e-05
gb AF039268.1 AF039268	Agkistrodon constrictor cytochrome b ...	50	2e-05
gb AF039267.1 AF039267	Boa constrictor cytochrome b (cytb) ...	50	2e-05
gb S49215.1 S49215	apocytochrome b (sheep, domestic, Merino...)	50	2e-05
gb AF158698.1 AF158698	Geomys pinetis cytochrome b gene, co...	50	2e-05
gb AF158692.1 AF158692	Geomys bursarius jugosicularis cyto...	50	2e-05
gb AF058193.1 AF058193	Ithaginis cruentus cytochrome b (cyt...)	50	2e-05
gb AF091629.1 AF091629	Antilocapra americana cytochrome b (...)	50	2e-05
gb AF022061.1	Tragelaphus strepsiceros cytochrome b (cytb) ...	50	2e-05
gb AF022052.1	Tragelaphus derbianus cytochrome b (cytb) ...	50	2e-05
gb AF022050.1	Hippotragus equinus cytochrome b (cytb) gene...	50	2e-05
gb AF022057.1	Tragelaphus oxyx cytochrome b (cytb) gene, m...	50	2e-05
gb AF111500.1 AF111500	Lagenostomus acutus isolate LACU74...	50	2e-05
gb AF111499.1 AF111499	Lagenostomus acutus isolate LACU75 ...	50	2e-05

gb U69463.1 LRU69463	Loxocemus bicolor cytochrome b (cytb) ...	50	2e-05
gb U69463.1 EIIU69463	Eunectes notaeus cytochrome b (cytb) 9...	50	2e-05
gb U69463.1 EMU69463	Eunectes murinus cytochrome b (cytb) 9...	50	2e-05
gb U69799.1 ESU69799	Epicrates striatus fosteri cytochrome ...	50	2e-05
gb U69799.1 ESU69799	Epicrates striatus strigilatus cytochr...	50	2e-05
gb U69799.1 ESU69799	Epicrates striatus strigilatus cytochr...	50	2e-05
gb U69799.1 ESU69799	Epicrates striatus mccraniei cytochrom...	50	2e-05
gb U69799.1 ESU69799	Epicrates striatus mccraniei cytochrom...	50	2e-05
gb U69799.1 EMU69799	Epicrates monensis cytochrome b (cytb) ...	50	2e-05
gb U69799.1 EMU69799	Epicrates monensis cytochrome b (cytb) ...	50	2e-05
cb U69786.1 EFU69786	Epicrates fordii cytochrome b (cytb) ge...	50	2e-05
gb U69784.1 EFU69784	Epicrates fordii cytochrome b (cytb) ge...	50	2e-05
gb U69779.1 ECU69779	Epicrates cenchria cytochrome b (cytb) ...	50	2e-05
gb U69777.1 ECU69777	Epicrates cenchria cytochrome b (cytb) ...	50	2e-05
gb U69776.1 EAU69776	Epicrates angulifer cytochrome b (cytb) ...	50	2e-05
gb U69774.1 EAU69774	Epicrates angulifer cytochrome b (cytb) ...	50	2e-05
cb U69772.1 CEU69772	Corallus enydris cytochrome b (cytb) 9...	50	2e-05
cb U69771.1 CEU69771	Corallus enydris cytochrome b (cytb) 9...	50	2e-05
gb U69770.1 CEU69770	Corallus enydris cytochrome b (cytb) 9...	50	2e-05
cb U69769.1 CEU69769	Corallus enydris cytochrome b (cytb) 9...	50	2e-05
cb U69752.1 CAU69752	Candoia aspera cytochrome b (cytb) gen...	50	2e-05
gb U69746.1 BCU69746	Boa constrictor cytochrome b (cytb) ge...	50	2e-05
gb U69740.1 BCU69740	Boa constrictor cytochrome b (cytb) ge...	50	2e-05
cb AF139057.1 AF139057	Isoodon macrourus cytochrome b gene, ...	50	2e-05
gb AF090339.1 AF090339	Rhea americana mitochondrial, comple...	50	2e-05
cb AF006275.1 AF006275	Cnemidophorus tigris strain Isla Ang...	50	2e-05
cb AF006267.1 AF006267	Cnemidophorus tigris strain Isla Smi...	50	2e-05
gb AF034969.1 AF034969	Conniochaetes tauminus cytochrome b 9...	50	2e-05
cb AF028822.1 AF028822	Alcelaphus buselaphus cytochrome b 9...	50	2e-05
cb AF028821.1 AF028821	Damaliscus lunatus cytochrome b gene...	50	2e-05
gb AF061340.1 AF061340	Artibeus jamaicensis mitochondrial D...	50	2e-05
cb AF076093.1 AF076093	Thalassarche impavida cytochrome b (...	50	2e-05
cb AF076091.1 AF076091	Thalassarche carteri cytochrome b (c...	50	2e-05
cb AF076072.1 AF076072	Pelagodroma marina cytochrome b (cyt...	50	2e-05
cb AF076063.1 AF076063	Oceanodroma furcata cytochrome b (cy...	50	2e-05
cb AF076059.1 AF076059	Hydrobates pelagicus cytochrome b (c...	50	2e-05
cb AF076056.1 AF076056	Garrodia nereis cytochrome b (cytb) ...	50	2e-05
gb AF076053.1 AF076053	Fregetta tropica cytochrome b (cytb) ...	50	2e-05
cb AF076050.1 AF076050	Diomedea gibsoni cytochrome b (cytb) ...	50	2e-05
gb AF076049.1 AF076049	Diomedea epomophora cytochrome b (cy...	50	2e-05
cb AF076048.1 AF076048	Diomedea chionoptera cytochrome b (c...	50	2e-05
cb AF076047.1 AF076047	Diomedea antipodensis cytochrome b (...	50	2e-05
gb U83314.1 MSU83314	Micrastur semitorquatus cytochrome b (...	50	2e-05
cb U83318.1 MEU83318	Microhierax erythrogenys cytochrome b ...	50	2e-05
cb U37303.1 SAU37303	Synthliboramphus antiquus cytochrome b...	50	2e-05
gb U37302.1 PAU37302	Psychoramphus aleuticus cytochrome b 9...	50	2e-05
cb U37295.1 CPU37295	Cyclorrhynchus psittacula cytochrome b...	50	2e-05
gb U37289.1 BBU37289	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb U37286.1 APU37286	Aethia pygmaea cytochrome b gene, mito...	50	2e-05
gb U37104.1 APU37104	Aethia pusilla cytochrome b gene, mito...	50	2e-05
gb U37087.1 ACU37087	Aethia cristatella cytochrome b gene, ...	50	2e-05
gb U87525.1 HGU87525	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb U87524.1 HGU87524	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb U87523.1 HGU87523	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb U87522.1 HGU87522	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb U17864.1 STU17864	Saiga tatarica cytochrome b gene, mito...	50	2e-05
gb U17863.1 OAU17863	Oreamnos americanus cytochrome b gene...	50	2e-05
gb U17862.1 OMU17862	Ovibos moschatus moschatus cytochrome ...	50	2e-05
gb U17860.1 ODU17860	Ovis dalli cytochrome b gene, mitochon...	50	2e-05
gb U17859.1 OCU17859	Ovis canadensis cytochrome b gene, mit...	50	2e-05
gb U65274.1 TBU65274	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb U65267.1 TBU65267	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb U65260.1 TBU65260	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb U65301.1 PAU65301	Perognathus amplus cytochrome b (cytb) ...	50	2e-05
gb AF034739.1 AF034739	Capra aegagrus cytochrome b (cytb) 3...	50	2e-05
gb AF034739.1 Capra caucasica	Capra caucasica cytochrome b (cytb) gene, mi...	50	2e-05
gb AF034739.1 Capra cylindricornis	Capra cylindricornis cytochrome b (cytb) gen...	50	2e-05
gb AF034739.1 Capra falconeri	Capra falconeri cytochrome b (cytb) ...	50	2e-05
gb AF034739.1 Capra ibex	Capra ibex cytochrome b (cytb) gene, mitochon...	50	2e-05
gb AF034739.1 Capra arietis	Ovis aries cytochrome b (cytb) gene, ...	50	2e-05
gb AF034739.1 Capra vignei	Ovis vignei cytochrome b (cytb) gene, ...	50	2e-05

gb AF034734.1	Ovis dalli dalli cytochrome b (cytb) gene, m...	50	2e-05
gb AF034737.1	Ovis ammon darwini cytochrome b (cytb) gene...	50	2e-05
gb AF034734.1 AF034724	Pantholops hodgsoni cytochrome b (cytb) ge...	50	2e-05
gb AF057131.1 AF057132	Taxidea taxus cytochrome b (cytb) gene...	50	2e-05
gb U94805.1 TMU94805	Trogon melanurus cytochrome b gene, mito...	50	2e-05
gb U94804.1 TCU94804	Trogon comptus cytochrome b gene, mito...	50	2e-05
gb U94803.1 TVU94803	Trogon viridis cytochrome b gene, mito...	50	2e-05
gb AF006251.1 AF006251	Sericossypha albocristata cytochrome...	50	2e-05
gb AF006249.1 AF006249	Pyrrhocoma ruficeps cytochrome b (cy...	50	2e-05
gb AF006238.1 AF006238	Lamprospiza melanoleuca cytochrome b...	50	2e-05
gb AF006234.1 AF006234	Hemispingus acropileus cytochrome b ...	50	2e-05
gb AF005226.1 AF006226	Cypsnagra hirundinacea cytochrome b ...	50	2e-05
gb AF006215.1 AF006215	Chlorophanes spiza cytochrome b (cyt...	50	2e-05
gb AF006214.1 AF006214	Chlorochrysa calliparaea cytochrome ...	50	2e-05
gb AF006213.1 AF006213	Calochaetes coccineus cytochrome b (...)	50	2e-05
gb AF006212.1 AF006212	Buchraupis montana cytochrome b (cyt...	50	2e-05
emb AJ293419.1 RRU293419	Rupicapra rupicapra rupicapra mito...	50	2e-05
emb AJ293416.1 RPPY293416	Rupicapra pyrenaica pyrenaica mito...	50	2e-05
emb AJ293415.1 RPPY293415	Rupicapra pyrenaica parva mitochon...	50	2e-05
emb AJ293414.1 RPPY293414	Rupicapra pyrenaica ornata mitochon...	50	2e-05
emb AJ293412.1 RRU293412	Rupicapra rupicapra rupicapra mito...	50	2e-05
emb AJ293418.1 CFA293418	Capra falconeri mitochondrial part...	50	2e-05
gb U07578.1 DCU07578	Dasyercus cristicauda mitochondrial c...	50	2e-05
emb AJ004180.1 HPAJ4180	Hydrobates pelagicus mitochondrial ...	50	2e-05
emb Y15695.1 SMY15695	Schilbe myrus mitochondrial cytb gen...	50	2e-05
emb Y15697.1 EDV15697	Eutropius depressirostris mitochondrial...	50	2e-05
emb Y15696.1 EDY15696	Eutropius depressirostris mitochondrial...	50	2e-05
gb AF015039.1 AF015035	Steatocranus casuarius 20 cytochrom...	50	2e-05
gb AF015761.1 AF015761	Palmaria dolei cytochrome b (Cytb) g...	50	2e-05
gb AF015758.1 AF015758	Oreomystis mana cytochrome b (Cytb) ...	50	2e-05
gb AF015756.1 AF015756	Vestiaria coccinea cytochrome b (Cyt...	50	2e-05
gb AF015754.1 AF015754	Himatione sanguinea cytochrome b (Cy...	50	2e-05
gb U76052.1 DNU76052	Dromaius novaehollandiae cytochrome b ...	50	2e-05
emb AJ236634.1 CGL236834	Clethrionomys glareolus mitochondrial...	50	2e-05
gb U83158.1 POU83158	Pelecanus onocrotalus cytochrome B gen...	50	2e-05
gb U83157.1 POU83157	Pelecanus onocrotalus cytochrome B gen...	50	2e-05
gb U83156.1 AAU83156	Anhinga anhinga cytochrome B gene, mit...	50	2e-05
gb U83155.1 AAU83155	Anhinga anhinga cytochrome B gene, mit...	50	2e-05
gb U83154.1 AAU83154	Anhinga anhinga cytochrome B gene, mit...	50	2e-05
gb U81356.1 CLUB1356	Chelodina longicollis cytochrome b gen...	50	2e-05
emb AJ277676.1 ESC277676	Elaphe scalaris mitochondrial part...	50	2e-05
emb AJ277675.1 ESC277675	Elaphe scalaris mitochondrial part...	50	2e-05
emb AJ277672.1 ELO277672	Elaphe longissima mitochondrial pa...	50	2e-05
emb AJ277671.1 ELO277671	Elaphe longissima mitochondrial pa...	50	2e-05
emb Y11832.1 MTDNCOMGN	Dasypus novemcinctus complete mitoch...	50	2e-05
emb AJ388467.1 NEA388467	Nemacheilus barbatus mitochondria...	50	2e-05
emb AJ388468.1 IME388468	Ictalurus melas mitochondrial cyt b...	50	2e-05
emb AJ388459.1 LDE388459	Leucaspis delineatus mitochondrial...	50	2e-05
gb U46167.1 SCU46167	Sciurus carolinensis cytochrome b gene...	50	2e-05
emb AJ245573.1 SIN245573	Schilbe intermedius partial mitoch...	50	2e-05
emb AJ245538.1 SIN245538	Schilbe intermedius partial mitoch...	50	2e-05
emb AJ245678.1 EDE245678	Eutropius depressirostris partial ...	50	2e-05
emb AJ245577.1 EDE245577	Eutropius depressirostris partial ...	50	2e-05
emb AJ245576.1 EDE245576	Eutropius depressirostris partial ...	50	2e-05
emb AJ245575.1 EDE245575	Eutropius depressirostris partial ...	50	2e-05
emb AJ245674.1 EDE245674	Eutropius depressirostris partial ...	50	2e-05
emb Y16884.3 MTRACOMP4	Rhea americana complete mitochondrial...	50	2e-05
gb U60768.1 PCU60768	Parus cinctus cytochrome b gene, mitoc...	50	2e-05
gb U48255.1 TMU48255	Thalassarche melanophris melanophris c...	50	2e-05
gb U48954.1 TCU48954	Thalassarche chrysostoma cytochrome b ...	50	2e-05
gb U48944.1 TCU48944	Thalassarche chlorostethos chlorosteth...	50	2e-05
gb U48343.1 PPU48343	Phoebebetria palpebrata cytochrome b (cy...	50	2e-05
gb U48942.1 PFU48942	Phoebebetria fusca cytochrome b (cytb) g...	50	2e-05
gb U48941.1 MGU48941	Macronectes giganteus cytochrome b (cy...	50	2e-05
gb U48947.1 DEU48947	Diomedea exulans dabbenena cytochrome ...	50	2e-05
gb U48746.1 DEU48746	Diomedea epomophora sanfordi cytochrom...	50	2e-05
gb U48749.1 DAU48749	Diomedea Amsterdamensis cytochrome b (...)	50	2e-05
gb U48575.1 PRU48575	Piranga rubra cytochrome b gene, mitoc...	50	2e-05
gb U55508.1 APU55508	Astibes planirostris cytochrome b (cy...	50	2e-05
gb U55507.1 ADU55507	Astibes obscurus cytochrome b (cytb) ...	50	2e-05
gb U55506.1 AOU55506	Astibes obscurus cytochrome b (cytb) ...	50	2e-05

gb U66505.1 ALUCCS05	<i>Aribeus hirsutus</i> cytochrome b (cytb) ...	50	2e-05
gb U66504.1 AJU66504	<i>Aribeus jamaicensis</i> cytochrome b (cyt...)	50	2e-05
gb U66503.1 AJU66503	<i>Aribeus jamaicensis</i> cytochrome b (cyt...)	50	2e-05
gb U66502.1 AIU66502	<i>Aribeus intermedius</i> cytochrome b (cyt...)	50	2e-05
gb U66501.1 AU66501	<i>Aribeus inopinatus</i> cytochrome b (cytb...)	50	2e-05
gb U66500.1 AHU66500	<i>Aribeus hirsutus</i> cytochrome b (cytb) ...	50	2e-05
gb U66499.1 AFU66499	<i>Aribeus fraterculus</i> cytochrome b (cyt...)	50	2e-05
gb U66498.1 AFU66498	<i>Aribeus fimbriatus</i> cytochrome b (cytb...)	50	2e-05
gb U61061.1 BBU63061	<i>Brachyramphus brevirostris</i> cytochrome ...	50	2e-05
gb U63060.1 BBU63060	<i>Brachyramphus brevirostris</i> cytochrome ...	50	2e-05
gb U63059.1 BBU63059	<i>Brachyramphus brevirostris</i> cytochrome ...	50	2e-05
gb U63058.1 BBU63058	<i>Brachyramphus brevirostris</i> cytochrome ...	50	2e-05
gb U58386.1 SJUS8386	<i>Scolomys juruaense</i> cytochrome b (cyt-b...)	50	2e-05
gb L11905.1 CGYMTCYTB	<i>Cratogeomys gunnurus</i> mitochondrial c...	50	2e-05
gb U34672.1 MNU34672	<i>Metachirus nudicaudatus</i> cytochrome b l...	50	2e-05
gb U34671.1 MNU34671	<i>Metachirus nudicaudatus</i> cytochrome b l...	50	2e-05
emb Y14951.1 MTY14951	<i>Capreolus capreolus</i> mitochondrial cyt...	50	2e-05
emb Y14371.1 MTCCCCYT	<i>Capreolus capreolus</i> mitochondrial cyt...	50	2e-05
gb L11909.1 CGYMTCYTBH	<i>Cratogeomys taylorinus</i> mitochondrial...	50	2e-05
gb L11901.1 PPGMYTCYTBB	<i>Geomys bursarius</i> jugosiculatus mito...	50	2e-05
gb L11904.1 CGYMTCYTB	<i>Cratogeomys goldmani</i> goldmani mitoch...	50	2e-05
emb X94928.1 SPFCYT	<i>S. putorius</i> mitochondrial DNA for cytoch...	50	2e-05
cb U46770.1 ARU46770	<i>Anthus richardi</i> cytochrome b gene, mit...	50	2e-05
cb U46769.1 ABU46769	<i>Anthus berthelotii</i> cytochrome b gene, ...	50	2e-05
cb U46183.1 SSU46183	<i>Sciurus stramineus</i> cytochrome b gene, ...	50	2e-05
emb Y10728.1 PSMY10728	<i>P. schwarzii</i> mitochondrial cytb gene, ...	50	2e-05
emb X95768.1 NLMCB	<i>N. leucopterus</i> mitochondrial cytochrome b...	50	2e-05
emb X95767.1 NGRIMCB	<i>N. griseus</i> mitochondrial cytochrome b gene	50	2e-05
emb X86763.1 MTVGCYT26	<i>V. gryphus</i> mitochondrial cytb gene	50	2e-05
emb X86754.1 MTLCCYT17	<i>L. crumeniferus</i> mitochondrial cytb gene	50	2e-05
emb X96743.1 MTCACYT6	<i>C. aura</i> mitochondrial cytb gene	50	2e-05
cbj A9035242.1 AB035242	<i>Pantodon buchholzi</i> mitochondrial cy...	50	2e-05
emb X50946.1 MITDCB33	<i>T. dorfignyi</i> mitochondrial gene for c...	50	2e-05
emb AJ000029.1 MIRTCB29	<i>Rangifer tarandus</i> mitochondrial cy...	50	2e-05
emb X82302.1 MIPFCYTBC	<i>P. fasciata</i> mitochondrial cytochrome ...	50	2e-05
emb X56291.1 MIOHCYT	<i>O. hemionus</i> mitochondrion cytb gene fo...	50	2e-05
emb X56284.1 MIOACYT	<i>O. aries</i> mitochondrion cytb gene for c...	50	2e-05
emb AJ000022.1 MIMSCYB22	<i>Dama dama</i> mitochondrial cytb gene	50	2e-05
emb X72005.1 MILWCYT	<i>L. weddelli</i> mitochondrial gene for cyt...	50	2e-05
emb Y09914.1 MIHLCYTB	<i>H. liberiensis</i> mitochondrial cytochro...	50	2e-05
emb X60942.1 MIGTCB33	<i>Gymnorhina tibicen</i> mitochondrial gene...	50	2e-05
emb X56290.1 MIDDCYT	<i>D. dama</i> mitochondrion cytb gene for cy...	50	2e-05
emb AJ000021.1 MICECYB21	<i>Cervus elaphus</i> mitochondrial cytb ...	50	2e-05
emb AJ000024.1 MICCCYB24	<i>Caprosolus caprosolus</i> mitochondrial ...	50	2e-05
emb V00654.1 MIETXX	<i>Bos taurus</i> complete mitochondrial genome	50	2e-05
emb X56286.1 MIAACYTBA	<i>A. americana</i> mitochondrion cytb gene ...	50	2e-05
cb L19718.1 AJUMTCYB	<i>Artibeus lituratus</i> mitochondrial cyto...	50	2e-05
cb U27543.1 BRU27543	<i>Balearica regulorum</i> cytochrome b (cytb...)	50	2e-05
cbj A9030025.1 AB030025	<i>Sciurus stramineus</i> mitochondrial cy...	50	2e-05
cb U18258.1 SCU18258	<i>Sparagemon campestris</i> cytochrome b ge...	50	2e-05
cb U18257.1 SCU18257	<i>Sparagemon coliare</i> cytochrome b gene...	50	2e-05
cb U18253.1 TPU18253	<i>Trimerotropis picturaria</i> cytochrome b...	50	2e-05
gb U18250.1 CPU18250	<i>Cannula pellucida</i> cytochrome b gene, m...	50	2e-05
gb U17904.1 CCU17904	<i>Circotettix carlinianus</i> mitochondrion ...	50	2e-05
cbj D84202.1 GOTMTCB8	<i>Capra falconeri</i> mitochondrial DNA for ...	50	2e-05
cbj D82889.1 D82889	<i>Bos javanicus</i> mitochondrial DNA for cyt...	50	2e-05
cbj D32195.1 CCRMTCB25	<i>Capricornis sumatrensis</i> mitochondrial...	50	2e-05
cbj D32191.1 CCRMTCB21	<i>Capricornis crispus</i> mitochondrial ge...	50	2e-05
cbj AB021098.1 AB021098	<i>Cervus elaphus kamsuensis</i> mitochondr...	50	2e-05
cbj AB021097.1 AB021097	<i>Cervus elaphus xanthopygus</i> mitochondr...	50	2e-05
cbj AB021095.1 AB021095	<i>Cervus nippon yesoensis</i> mitochondr...	50	2e-05
cbj AB021094.1 AB021094	<i>Cervus nippon centralis</i> mitochondr...	50	2e-05
cbj AB021092.1 AB021092	<i>Cervus nippon mugeshimae</i> mitochondr...	50	2e-05
cbj AB021091.1 AB021091	<i>Cervus nippon keramae</i> mitochondrial...	50	2e-05
cbj AB001612.1 AB001612	<i>Cervus elaphus</i> mitochondrial DNA fo...	50	2e-05
cbj D84205.1 SHPMTCB	Sheep mitochondrial DNA for cytochrom...	50	2e-05
cbj D84203.1 SHPMTCBC	<i>Ovis musimon</i> mitochondrial DNA for cyt...	50	2e-05
cbj D24516.1 BOVMTCB8	<i>Bos javanicus</i> mitochondrial gene for ...	50	2e-05
cbj D24515.1 BOVMTCB	<i>Bovine</i> mitochondrial gene for cytochr...	50	2e-05
cbj D24518.1 ORMMTCB8	<i>Oreamnos americanus</i> mitochondrial ge...	50	2e-05
cbj D24519.1 MACMTCB6	<i>Marmosaeus garsi</i> mitochondrial gene...	50	2e-05

dbj S321421.1 CEUMTCB12	Cervus nippon mitochondrial gene for...	50	2e-05
dbj A5021046.1 AB021094	Cervus elaphus scoticus mitochondrial...	50	2e-05
dbj A8021096.1 AB021096	Cervus elaphus canadensis mitochondrial...	50	2e-05
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dbj A8021090.1 AB021090	Cervus nippon pulchellus mitochondrial...	50	2e-05
dbj A8006535.1 AB006535	Dinodon semicarinatus mitochondrial...	50	2e-05
dbj AB006800.1 AB006800	Ovis aries mitochondrial DNA for cy...	50	2e-05
gb L13763.1 LDHMTCYB	Lepidochelys kempi (LK-3) mitochondrial...	50	2e-05
gb L06032.1 CP1MTCYB	Carcharhinus plumbeus mitochondrial ...	50	2e-05
gb L28941.1 URCYS	Uroderma bilobatum cytochrome b gene, 5'...	50	2e-05
gb L28937.1 CDECYB	Chiropus dorsae cytochrome b gene, 5' end	50	2e-05
emb AJ010056.1 CPY010056	Capra pyrenaica (individual 12) mi...	50	2e-05
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emb AJ010053.1 CPY010053	Capra pyrenaica (individual 10) mi...	50	2e-05
emb AJ010052.1 CPY010052	Capra pyrenaica (individual 9) mit...	50	2e-05
emb AJ010051.1 CPY010051	Capra pyrenaica (individual 8) mit...	50	2e-05
emb AJ010050.1 CPY010050	Capra pyrenaica (individual 7) mit...	50	2e-05
emb AJ010049.1 CPY010049	Capra pyrenaica (individual 6) mit...	50	2e-05
emb AJ010048.1 CPY010048	Capra pyrenaica (individual 5) mit...	50	2e-05
emb AJ010047.1 CPY010047	Capra pyrenaica (individual 4) mit...	50	2e-05
emb X95777.1 CLMCE	C. longirostris mitochondrial cytochrome ...	50	2e-05
emb AJ009279.1 CIB39879	Capra ibex nubiana mitochondrial cyt...	50	2e-05
emb AJ010055.1 CTB010055	Capra ibex (individual 1) ibex mit...	50	2e-05
gb U08946.1 CAU08946	Coragyps atratus mitochondrion cytochr...	50	2e-05
gb U08945.1 CBU08945	Cathartes burrovianus mitochondrion cy...	50	2e-05
gb U08944.1 VGU08944	Vultur gryphus mitochondrion cytochrom...	50	2e-05
cb U08941.1 PAU08941	Platalea alba mitochondrion cytochrome...	50	2e-05
gb U08940.1 PRU08940	Phoenicopterus ruber mitochondrion cyt...	50	2e-05
emb X95775.1 ACMCB	A. cristatus mitochondrial cytochrome b gene	50	2e-05
emb X95774.1 ABMCB	A. bennettii mitochondrial cytochrome b gene	50	2e-05
emb X95764.1 AAMCB	A. albertisi mitochondrial cytochrome b gene	50	2e-05
cb AF040383.1 AF040383	Alces alces cytochrome b (cytb) gene...	45	3e-04
cb AF232023.1 AF232023	Tamandua tetradactyla clone 7 cytoch...	45	3e-04
gb AF232022.1 AF232022	Tamandua tetradactyla clone 6 mitoch...	45	3e-04
cb AF232021.1 AF232021	Tamandua tetradactyla clone 5 cytoch...	45	3e-04
cb AF157466.1 AF157466	Lepus timidus cytochrome b (Cyb) gen...	45	3e-04
cb AF157465.1 AF157465	Lepus granatensis cytochrome b (Cyb)...	45	3e-04
cb AF157454.1 AF157464	Lepus corsicanus haplotype 1 cytochr...	45	3e-04
cb AF157453.1 AF157463	Lepus corsicanus haplotype 3 cytochr...	45	3e-04
cb AF157450.1 AF157460	Lepus europaeus cytochrome b (Cyb) g...	45	3e-04
cb AF231664.1 AF231664	Tylosurus crocodilus crocodilus cyto...	45	3e-04
cb AF231663.1 AF231663	Tylosurus crocodilus cline STRI-1617...	45	3e-04
gb AF231662.1 AF231662	Tylosurus crocodilus clone KB-166 cy...	45	3e-04
gb AF231660.1 AF231660	Tylosurus acus pacificus cytochrome ...	45	3e-04
gb AF231659.1 AF231659	Tylosurus acus melanotus clone STRI-...	45	3e-04
gb AF231658.1 AF231658	Tylosurus acus melanotus clone STRI-...	45	3e-04
cb AF231657.1 AF231657	Tylosurus acus imperialis cytochrome...	45	3e-04
gb AF231656.1 AF231656	Tylosurus acus acus cytochrome b cxi...	45	3e-04
gb AF231644.1 AF231644	Strongylura hubbsi cytochrome b oxid...	45	3e-04
gb AF231639.1 AF231639	Ablennes hians cytochrome b oxidase ...	45	3e-04
gb AF232019.1 AF232019	Tamandua tetradactyla clone 3 cytoch...	45	3e-04
gb AF232017.1 AF232017	Tamandua tetradactyla clone 1 cytoch...	45	3e-04
gb AF232014.1 AF232014	Mylodon darwini cytochrome b gene. ...	45	3e-04
gb AF318554.1 AF318564	Alligator mississippiensis isolate S...	45	3e-04
gb AF318553.1 AF318563	Alligator mississippiensis isolate S...	45	3e-04
gb AF318562.1 AF318562	Alligator mississippiensis isolate S...	45	3e-04
gb AF318561.1 AF318561	Alligator mississippiensis isolate G...	45	3e-04
gb AF318560.1 AF318560	Alligator mississippiensis isolate G...	45	3e-04
gb AF318559.1 AF318559	Alligator mississippiensis isolate A...	45	3e-04
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gb AF318550.1 AF318550	Alligator mississippiensis isolate F...	45	3e-04
gb AF318549.1 AF318549	Alligator mississippiensis isolate F...	45	3e-04
gb AF318548.1 AF318548	Alligator mississippiensis isolate F...	45	3e-04
gb AF318041.1 AF318041	Sorex monticolus specimen-voucher AF...	45	3e-04

<u>gb AF326272.1 AF326272</u>	Myospalax myospalax cytochrome b (cy... isolate 2 cytochr...	<u>46</u>	<u>3e-04</u>
<u>gb AF326271.1 AF326271</u>	Myospalax psilurus isolate 2 cytochr...	<u>46</u>	<u>3e-04</u>
<u>gb AF326270.1 AF326270</u>	Myospalax psilurus isolate 1 cytochr...	<u>46</u>	<u>3e-04</u>
<u>gb AF326266.1 AF326266</u>	Eospalax fontanieri isolate 4 cytoc...	<u>46</u>	<u>3e-04</u>
<u>emb AJ004340.1 ADAJ4340</u>	Acrocephalus dumetorum mitochondria...	<u>44</u>	<u>0.001</u>
<u>emb AJ004264.1 ADAJ4264</u>	Acrocephalus dumetorum mitochondria...	<u>44</u>	<u>0.001</u>

## Alignments

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<u>AF310052</u>	299	.	323
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<u>AF171919</u>	302	.	326
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<u>AF290174</u>	281	.	305
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<u>AF163904</u>	398	.	422
<u>AF163901</u>	398	.	422
<u>AF163899</u>	398	.	422
<u>AF163891</u>	398	.	422
<u>AF163890</u>	398	.	422
<u>AF288524</u>	401	.	425
<u>AF288523</u>	401	.	425
<u>AF288522</u>	401	.	425
<u>AF121510</u>	303	.	327
<u>AF121512</u>	301	.	327
<u>AF206548</u>	301	.	327
<u>AF197867</u>	401	.	425
<u>U61197</u>	303	.	327
<u>NC_001945</u>	15302	.	15326

<u>NC_001821</u>	14568	.....	14592
<u>AF141217</u>	398	.....	422
<u>AF201615</u>	385	.....	409
<u>AF077920</u>	154	.....	178
<u>AF190632</u>	398	.....	422
<u>J01394</u>	14911	.....	14935
<u>AF193830</u>	302	.....	326
<u>U89181</u>	401	.....	425
<u>U89171</u>	401	.....	425
<u>AF217833</u>	371	.....	395
<u>AF217822</u>	374	.....	398
<u>AF217813</u>	374	.....	398
<u>AF220408</u>	413	.....	437
<u>AF126430</u>	398	.....	422
<u>AF090337</u>	15123	.....	15147
<u>AF059111</u>	305	.....	329
<u>AF059053</u>	305	.....	329
<u>AF099308</u>	303	.....	327
<u>AF099295</u>	303	.....	327
<u>AF099294</u>	303	.....	327
<u>AF099293</u>	303	.....	327
<u>AF160610</u>	398	.....	422
<u>AF036280</u>	398	.....	422
<u>AF036277</u>	398	.....	422
<u>AF036274</u>	398	.....	422
<u>AF194218</u>	302	.....	326
<u>AF194216</u>	302	.....	326
<u>NC_002009</u>	14547	.....	14571
<u>NC_001941</u>	14556	.....	14580
<u>NC_000877</u>	15123	.....	15147
<u>NC_000846</u>	14038	.....	14062
<u>U27551</u>	401	.....	425
<u>AF089058</u>	281	.....	305
<u>AF089055</u>	281	.....	305
<u>AF089054</u>	281	.....	305
<u>AF089046</u>	281	.....	305
<u>AF089042</u>	272	.....	296
<u>AF089039</u>	281	.....	305
<u>AF089037</u>	281	.....	305
<u>AF089026</u>	281	.....	305
<u>AF089025</u>	281	.....	305
<u>AF089024</u>	281	.....	305
<u>AF089023</u>	281	.....	305
<u>AF089021</u>	281	.....	305
<u>AF089020</u>	281	.....	305
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<u>AF089013</u>	281	.....	305
<u>AF089012</u>	281	.....	305
<u>AF089008</u>	281	.....	305
<u>AF089006</u>	257	.....	281
<u>AF089005</u>	281	.....	305
<u>AF108696</u>	398	.....	422
<u>AF108685</u>	392	.....	416
<u>AF108677</u>	398	.....	422
<u>AF145531</u>	169	.....	193
<u>AF145511</u>	169	.....	193
<u>U89627</u>	360	.....	384
<u>U89623</u>	360	.....	384
<u>AF181470</u>	303	.....	327
<u>AF084075</u>	398	.....	422
<u>U90301</u>	398	.....	422
<u>U90302</u>	398	.....	422
<u>U90301</u>	398	.....	422
<u>U90300</u>	398	.....	422
<u>AF018881</u>	392	.....	416
<u>AF019268</u>	392	.....	416
<u>AF019257</u>	392	.....	416
<u>S19215</u>	56	.....	80
<u>AF138698</u>	398	.....	422
<u>AF138693</u>	398	.....	422
<u>AF0768121</u>	401	.....	425

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<u>AF022063</u>	398	.....	422
<u>AF022062</u>	398	.....	422
<u>AF022060</u>	398	.....	422
<u>AF022057</u>	398	.....	422
<u>AF113500</u>	384	.....	408
<u>AF113499</u>	363	.....	387
<u>U69845</u>	374	.....	398
<u>U69810</u>	374	.....	398
<u>U69808</u>	374	.....	398
<u>U69799</u>	374	.....	398
<u>U69796</u>	374	.....	398
<u>U69795</u>	374	.....	398
<u>U69794</u>	374	.....	398
<u>U69793</u>	374	.....	398
<u>U69792</u>	374	.....	398
<u>U69790</u>	374	.....	398
<u>U69786</u>	374	.....	398
<u>U69784</u>	374	.....	398
<u>U69779</u>	374	.....	398
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<u>U69776</u>	374	.....	398
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<u>U69771</u>	374	.....	398
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<u>U69769</u>	374	.....	398
<u>U69752</u>	74	.....	98
<u>U69746</u>	374	.....	398
<u>U69740</u>	374	.....	398
<u>AF139057</u>	398	.....	422
<u>AF090339</u>	15199	.....	15223
<u>AF006275</u>	475	.....	499
<u>AF006267</u>	475	.....	499
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<u>AF028822</u>	398	.....	422
<u>AF028821</u>	398	.....	422
<u>AF061340</u>	14547	.....	14571
<u>AF076093</u>	401	.....	425
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<u>AF076063</u>	401	.....	425
<u>AF076059</u>	401	.....	425
<u>AF076056</u>	401	.....	425
<u>AF076053</u>	401	.....	425
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<u>AF076049</u>	401	.....	425
<u>AF076048</u>	401	.....	425
<u>AF076047</u>	401	.....	425
<u>U83314</u>	401	.....	425
<u>U83318</u>	401	.....	327
<u>U37303</u>	303	.....	327
<u>U37302</u>	303	.....	327
<u>U37296</u>	303	.....	327
<u>U37289</u>	303	.....	327
<u>U37286</u>	303	.....	327
<u>U37104</u>	303	.....	327
<u>U37087</u>	303	.....	327
<u>U87525</u>	380	.....	404
<u>U87524</u>	385	.....	409
<u>U87523</u>	354	.....	378
<u>U87522</u>	379	.....	403
<u>U17864</u>	398	.....	422
<u>U17861</u>	329	.....	353
<u>U17862</u>	398	.....	422
<u>U17860</u>	398	.....	422
<u>U17859</u>	329	.....	353
<u>U65274</u>	398	.....	422
<u>U65267</u>	398	.....	422
<u>U65269</u>	398	.....	422
<u>U65191</u>	178	.....	422

<u>AF034739</u>	398	.	422
<u>AF034738</u>	398	.	422
<u>AF034737</u>	398	.	422
<u>AF034736</u>	398	.	422
<u>AF034735</u>	398	.	422
<u>AF034730</u>	398	.	422
<u>AF034729</u>	398	.	422
<u>AF034728</u>	398	.	422
<u>AF034727</u>	398	.	422
<u>AF034724</u>	398	.	422
<u>AF057132</u>	396	.	422
<u>U94805</u>	401	.	425
<u>U94804</u>	401	.	425
<u>U94803</u>	401	.	425
<u>AF006251</u>	303	.	327
<u>AF006249</u>	303	.	327
<u>AF006238</u>	303	.	327
<u>AF006234</u>	303	.	327
<u>AF006226</u>	303	.	327
<u>AF006215</u>	303	.	327
<u>AF006214</u>	303	.	327
<u>AF006213</u>	303	.	327
<u>AF006212</u>	303	.	327
<u>AJ293419</u>	398	.	422
<u>AJ293416</u>	398	.	422
<u>AJ293415</u>	398	.	422
<u>AJ293414</u>	398	.	422
<u>AJ293412</u>	398	.	422
<u>AJ293418</u>	398	.	422
<u>U07578</u>	398	.	422
<u>AJ004180</u>	302	.	326
<u>Y15695</u>	432	.	456
<u>Y15697</u>	432	.	456
<u>Y15696</u>	432	.	472
<u>AF015035</u>	448	.	327
<u>AF015761</u>	303	.	327
<u>AF015758</u>	303	.	327
<u>AF015756</u>	303	.	327
<u>AF015754</u>	303	.	327
<u>U76052</u>	401	.	425
<u>AJ236834</u>	398	.	422
<u>U83158</u>	302	.	326
<u>U83157</u>	304	.	328
<u>U83156</u>	302	.	326
<u>U83155</u>	303	.	327
<u>U83154</u>	300	.	324
<u>U81356</u>	320	.	324
<u>AJ277676</u>	299	.	323
<u>AJ277675</u>	299	.	323
<u>AJ277672</u>	299	.	323
<u>AJ277671</u>	299	.	323
<u>Y11832</u>	14568	.	14592
<u>AJ388457</u>	305	.	329
<u>AJ388468</u>	305	.	329
<u>AJ388459</u>	305	.	329
<u>U46167</u>	398	.	422
<u>AJ245673</u>	400	.	424
<u>AJ245678</u>	400	.	424
<u>AJ245678</u>	400	.	424
<u>AJ245677</u>	400	.	424
<u>AJ245676</u>	400	.	424
<u>AJ245675</u>	400	.	424
<u>AJ245674</u>	400	.	424
<u>Y16884</u>	14038	.	14062
<u>U60769</u>	243	.	267
<u>U48955</u>	401	.	425
<u>U48954</u>	401	.	425
<u>U48944</u>	401	.	425
<u>U48941</u>	401	.	425
<u>U48942</u>	401	.	425
<u>U48941</u>	401	.	425

<u>U48947</u>	401	.....	425
<u>U48946</u>	401	.....	425
<u>U48948</u>	401	.....	425
<u>U15725</u>	303	.....	327
<u>U56508</u>	398	.....	422
<u>U56507</u>	398	.....	422
<u>U66506</u>	398	.....	422
<u>U66505</u>	398	.....	422
<u>U66504</u>	398	.....	422
<u>U66503</u>	398	.....	422
<u>U66502</u>	398	.....	422
<u>U66501</u>	398	.....	422
<u>U66500</u>	398	.....	422
<u>U66499</u>	398	.....	422
<u>U66498</u>	398	.....	422
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<u>U63059</u>	302	.....	326
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<u>U58386</u>	398	.....	422
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<u>U34672</u>	398	.....	422
<u>U34671</u>	398	.....	422
<u>Y14951</u>	398	.....	422
<u>Y14371</u>	398	.....	422
<u>L11909</u>	398	.....	422
<u>L11901</u>	398	.....	422
<u>L11904</u>	398	.....	422
<u>X94928</u>	398	.....	422
<u>U46770</u>	302	.....	326
<u>U46769</u>	302	.....	326
<u>U46183</u>	398	.....	422
<u>Y10728</u>	299	.....	323
<u>X95768</u>	303	.....	327
<u>X95767</u>	303	.....	323
<u>X86763</u>	299	.....	323
<u>X86754</u>	299	.....	323
<u>X86743</u>	299	.....	323
<u>AB035242</u>	398	.....	422
<u>X60946</u>	302	.....	326
<u>AJ000029</u>	398	.....	422
<u>X82302</u>	398	.....	422
<u>X56291</u>	398	.....	422
<u>X56284</u>	398	.....	422
<u>AJ000022</u>	398	.....	422
<u>X72005</u>	398	.....	422
<u>Y08814</u>	398	.....	326
<u>X60942</u>	302	.....	422
<u>X56290</u>	398	.....	422
<u>AJ000021</u>	398	.....	422
<u>AJ000024</u>	398	.....	422
<u>V00654</u>	14911	.....	14935
<u>X56286</u>	398	.....	422
<u>L19718</u>	398	.....	422
<u>U27543</u>	401	.....	367
<u>AB030025</u>	343	.....	193
<u>U18258</u>	169	.....	193
<u>U18257</u>	169	.....	193
<u>U18253</u>	169	.....	193
<u>U18250</u>	169	.....	193
<u>U17904</u>	169	.....	193
<u>D84202</u>	398	.....	422
<u>D82882</u>	398	.....	422
<u>D12195</u>	243	.....	267
<u>D12191</u>	398	.....	422
<u>AB021098</u>	398	.....	422
<u>AB021097</u>	398	.....	422
<u>AB021095</u>	398	.....	422
<u>AB021094</u>	398	.....	422
<u>AB021092</u>	398	.....	422
<u>AB021091</u>	398	.....	422

<u>A8001612</u>	398	.	422
<u>D84205</u>	398	.	422
<u>D84203</u>	398	.	422
<u>D34636</u>	398	.	422
<u>D34615</u>	398	.	267
<u>D32198</u>	243	.	267
<u>D32196</u>	243	.	422
<u>D32192</u>	398	.	422
<u>AB021099</u>	398	.	422
<u>AB021096</u>	398	.	422
<u>AB021093</u>	398	.	422
<u>AB021090</u>	398	.	422
<u>AB008539</u>	15302	.	15326
<u>AB006800</u>	398	.	422
<u>L12763</u>	260	.	284
<u>L08032</u>	401	.	425
<u>L28941</u>	398	.	422
<u>L28937</u>	398	.	422
<u>AJ010056</u>	269	.	293
<u>AJ010054</u>	269	.	293
<u>AJ010053</u>	269	.	293
<u>AJ010052</u>	269	.	293
<u>AJ010051</u>	269	.	293
<u>AJ010050</u>	269	.	293
<u>AJ010049</u>	269	.	293
<u>AJ010048</u>	269	.	293
<u>AJ010047</u>	269	.	293
<u>X95777</u>	407	.	431
<u>AJ009879</u>	269	.	293
<u>AJ010055</u>	269	.	293
<u>U08946</u>	303	.	327
<u>U08945</u>	303	.	327
<u>U08944</u>	303	.	327
<u>Y08941</u>	303	.	327
<u>U08940</u>	303	.	327
<u>X95775</u>	303	.	327
<u>X95774</u>	303	.	327
<u>X95764</u>	303	.	310
<u>AF040383</u>	287	.	422
<u>AF232023</u>	400	.	422
<u>AF232022</u>	400	.	422
<u>AF232021</u>	400	.	422
<u>AF157466</u>	322	.	344
<u>AF157465</u>	324	.	346
<u>AF157464</u>	324	.	346
<u>AF157463</u>	324	.	346
<u>AF157460</u>	321	.	343
<u>AF231664</u>	400	.	422
<u>AF231663</u>	400	.	422
<u>AF231662</u>	400	.	422
<u>AF231660</u>	400	.	422
<u>AF231659</u>	400	.	422
<u>AF231658</u>	400	.	422
<u>AF231657</u>	400	.	422
<u>AF231656</u>	400	.	422
<u>AF231644</u>	400	.	422
<u>AF231639</u>	400	.	422
<u>AF232019</u>	400	.	422
<u>AF232017</u>	400	.	422
<u>AF232014</u>	400	.	422
<u>AF318564</u>	345	.	167
<u>AF318563</u>	345	.	167
<u>AF318562</u>	344	.	166
<u>AF318561</u>	344	.	166
<u>AF318560</u>	344	.	166
<u>AF318559</u>	344	.	166
<u>AF318558</u>	344	.	166
<u>AF318557</u>	381	.	163
<u>AF318556</u>	381	.	163
<u>AF318555</u>	381	.	163
<u>AF318554</u>	381	.	163

<u>AFJ18551</u>	381	.....	403
<u>AFJ18552</u>	381	.....	403
<u>AFJ18551</u>	381	.....	403
<u>AFJ18550</u>	381	.....	403
<u>AFJ18549</u>	381	.....	403
<u>AFJ18548</u>	381	.....	403
<u>AFJ28041</u>	400	.....	422
<u>AFJ26272</u>	400	.....	422
<u>AFJ26271</u>	400	.....	422
<u>AFJ26270</u>	400	.....	422
<u>AFJ26266</u>	400	.....	422
<u>AJ004340</u>	302	....n.....	326
<u>AJ004264</u>	302	....n.....	326

Database: nt

Posted date: Mar 2, 2001 12:20 AM

Number of letters in database: 2,863,827,885

Number of sequences in database: 807,597

Lambda K H  
1.37 0.711 1.31

Gapped

Lambda K H  
1.37 0.711 1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 39355

Number of Sequences: 807597

Number of extensions: 39355

Number of successful extensions: 15066

Number of sequences better than 10.0: 5706

length of query: 25

length of database: 2,863,827,885

effective HSP length: 17

effective length of query: 8

effective length of database: 2,850,098,736

effective search space: 22800789888

effective search space used: 22800789888

T: 0

A: 30

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 16 (32.2 bits)

**Table 11.** BLAST analysis of primers 'mcb869' in *nr* database of NCBI. It demonstrates that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer.

[BLASTN 2.1.2 \[Nov-13-2000\]](#)

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,  
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),  
"Gapped BLAST and PSI-BLAST: a new generation of protein database search  
programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593033-24247-14777

Query= (26 letters)

Database: nt  
807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQ's](#)

[Taxonomy reports](#)

Distribution of 500 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



## Sequences producing significant alignments:

		Score (bits)	S Value
gb AF189111.1 AF189111	Cryptotermes austrinus cytochrome b ...	52	6e-06
gb U86834.1 U86834	Phyllotis wolffsohni MS3 67270 cytochrom...	52	6e-06
gb AF123631.1 AF123631	Perissodipus tricolor cytochrome ...	52	6e-06
gb AF123617.1 AF123617	Pipreola arcuata cytochrome b gene, ...	52	6e-06
gb AF127202.1 AF127202	Hyloperus fulviventris cytochrome b ...	52	6e-06
gb AF127194.1 AF127194	Grallaria guatimalensis cytochrome b...	52	6e-06
gb AF217828.1 AF217828	Aspidelaps scutatus cytochrome b gen...	52	6e-06
gb AF160578.1 AF160578	Hypogeomys antimena Hant555 cytochro...	52	6e-06
gb AF009931.2 AF009931	Archocentrus centrarchus cytochrome ...	52	6e-06
gb AF091629.1 AF091629	Antilocapra americana cytochrome b (...)	52	6e-06
gb AF034967.1	Sigmoceros lichtensteinii cytochrome b gene, ...	52	6e-06
gb AF038290.1 AF038290	Antechinus sp. cytochrome b gene, mi...	52	6e-06
gb U07577.1 AMU07577	Antechinus melanurus mitochondrial cyt...	52	6e-06
gb U81343.1 CFU81343	Chelus fimbriata cytochrome b gene, mi...	52	6e-06
emb AJ222631.1 ABCYTB8	Alcelaphus buselaphus mitochondrial ...	52	6e-06
gb M99464.1 PNZMTCTB8	Planigale sp. cytochrome b gene, comp...	52	6e-06
emb AJ225116.1 DNJ225116	Dryomyz nitedula mitochondrial gen...	52	6e-06
gb U25738.1 PRU25738	Paradisaea raggiana cytochrome b gene, ...	52	6e-06
gb U25736.1 PRU25736	Paradisaea rubra cytochrome b gene, mi...	52	6e-06
gb U15202.1 SMU15202	Seleucidis melanoleuca mitochondrial c...	52	6e-06
gb U15204.1 PR15204	Paradisaea raggiana mitochondrial cytoc...	52	6e-06
emb X56290.1 MIDCYTB8	D.dama mitochondrial cytb gene for cy...	52	6e-06
emb X56286.1 MIAACYTB8	A.americana mitochondrial cytb gene ...	52	6e-06
dbj D88639.1 D88639	Anoa depressicornis mitochondrial DNA f...	52	6e-06
dbj D82890.1 D82890	Bubalus depressicornis mitochondrial DN...	52	6e-06
gb AF119261.1 AF119261	Peromyscus maniculatus cytochrome b ...	45	3e-04
gb AF123615.1 AF123615	Rupicola rupicola cytochrome b gene, ...	45	3e-04
gb AF160603.1 AF160603	Apodemus sylvaticus Asyl588 cytochro...	45	3e-04
gb U62697.1 CCOLCYTB2	Charadrius collaris cytochrome b (cyt...)	45	3e-04
gb U62685.1 CSICCYTB2	Charadrius bicinctus cytochrome b (cyt...)	45	3e-04
gb AF022071.1	Madoqua guentheri cytochrome b (cytb) gene, ...	45	3e-04
gb AF022070.1	Madoqua kirkii cytochrome b (cytb) gene, mit...	45	3e-04
gb U83317.1 PSU83317	Polihierax semitorquatus cytochrome b ...	45	3e-04
gb U37293.1 CCU37293	Cephus columba cytochrome b gene, mit...	45	3e-04
gb U37292.1 CCU37292	Cephus carbo cytochrome b gene, mitoc...	45	3e-04
gb U37291.1 BMU37291	Brachyramphus marmoratus perdix cytoch...	45	3e-04
gb AF082055.1 AF082055	Rupicola rupicola cytochrome b gene, ...	45	3e-04
gb U72770.1 JMU72770	Jabiru mycteria cytochrome b gene, mit...	45	3e-04
gb U07578.1 DCU07578	Dasyercus cristicauda mitochondrial c...	45	3e-04
gb AF031908.1 GOCCCYTB3	Geopsittacus occidentalis cytochrom...	45	3e-04
emb AJ004231.1 SBAJ4231	Sula bassana mitochondrial cytb gen...	45	3e-04
emb AJ004230.1 SBAJ4230	Sula bassana mitochondrial cytb gen...	45	3e-04
emb AJ004229.1 SBAJ4229	Sula bassana mitochondrial cytb gen...	45	3e-04
emb AJ004232.1 SBAJ4232	Sula bassana mitochondrial cytb gen...	45	3e-04
gb U88865.1	Pomacentrus sp. cytochrome b (cytb) gene, mito...	45	3e-04
gb U90001.1 MBU90001	Morus bassanus cytochrome b gene, mito...	45	3e-04
gb U63057.1 BMU63057	Brachyramphus marmoratus perdix cytoch...	45	3e-04
dbj AB036404.1 AB036404	Rana porosa brevipoda mitochondrial ...	45	3e-04
dbj AB036402.1 AB036402	Rana porosa brevipoda mitochondrial ...	45	3e-04
dbj AB036400.1 AB036400	Rana porosa brevipoda mitochondrial ...	45	3e-04
dbj AB036398.1 AB036398	Rana porosa porosa mitochondrial DN...	45	3e-04
gb U19611.1 JMU19611	Jabiru mycteria cytochrome b gene, mit...	45	3e-04
emb K92539.1 HACYTB8	H. ampullatus cytochrome b gene (complet...	45	3e-04
gb L08034.1 GAENTCYTB8	Galeocerdo cuvier mitochondrial cyto...	45	3e-04
gb L08033.1 CPLMTCTB8	Carcharhinus porosus mitochondrial c...	45	3e-04
gb AY015012.1	Crypturellus tacaupa mitochondrial, partial ...	44	0.001
gb AF074591.1 AF074591	Petrochelidon pyrrhonota cytochrome ...	44	0.001
gb AY005212.1	Pooospiza whitii isolate 2 cytochrome b (cytb...)	44	0.001
gb AY005211.1	Pooospiza whitii isolate 1 cytochrome b (cytb...)	44	0.001
gb AF189122.1 AF189122	Cryptococcomes coccineus cytochrome b ...	44	0.001
gb AF189120.1 AF189120	Cryptococcomes secundus cytochrome b (...)	44	0.001
gb AF189119.1 AF189119	Cryptococcomes primus isolate 2 cytoch...	44	0.001
gb AF189117.1 AF189117	Cryptococcomes primus isolate 1 cytoch...	44	0.001
gb AF189116.1 AF189116	Cryptococcomes dudleyi cytochrome b (Cy...)	44	0.001
gb AF122119.1 AF122119	Ovis canadensis cytochrome b gene, p ...	44	0.001
gb AF122117.1 AF122117	Ovis canadensis canadensis cytochrom...	44	0.001
gb AF122115.1 AF122115	Ovis canadensis neleoni cytochrome b ...	44	0.001
gb AF222122.1 AF222122	Vireo cassinii cassini apicalmen...	44	0.001

gb AF081989.1 AF081989	Vireo cassinii cassinii specimen-vou...	<u>44</u>	0.001
gb AF081988.1 AF081988	Vireo cassinii cassinii specimen-vou...	<u>44</u>	0.001
gb AF081987.1 AF081987	Vireo cassinii cassinii specimen-vou...	<u>44</u>	0.001
gb AF081986.1 AF081986	Vireo cassinii cassinii specimen-vou...	<u>44</u>	0.001
gb AF081985.1 AF081985	Vireo cassinii cassinii specimen-vou...	<u>44</u>	0.001
gb AF081984.1 AF081984	Vireo cassinii cassinii specimen-vou...	<u>44</u>	0.001
gb AF081983.1 AF081983	Vireo cassinii cassinii specimen-vou...	<u>44</u>	0.001
gb AF081982.1 AF081982	Vireo cassinii cassinii specimen-vou...	<u>44</u>	0.001
gb AF081981.1 AF081981	Vireo cassinii cassinii specimen-vou...	<u>44</u>	0.001
gb AF081980.1 AF081980	Vireo cassinii cassinii specimen-vou...	<u>44</u>	0.001
gb AF081979.1 AF081979	Vireo cassinii cassinii specimen-vou...	<u>44</u>	0.001
gb AF081978.1 AF081978	Vireo cassinii cassinii specimen-vou...	<u>44</u>	0.001
gb AF081977.1 AF081977	Vireo cassinii cassinii specimen-vou...	<u>44</u>	0.001
gb AF081976.1 AF081976	Vireo cassinii cassinii specimen-vou...	<u>44</u>	0.001
gb AF081975.1 AF081975	Vireo cassinii cassinii specimen-vou...	<u>44</u>	0.001
gb AF081974.1 AF081974	Vireo cassinii cassinii specimen-vou...	<u>44</u>	0.001
gb AF081973.1 AF081973	Vireo cassinii cassinii specimen-vou...	<u>44</u>	0.001
gb AF081972.1 AF081972	Vireo cassinii cassinii specimen-vou...	<u>44</u>	0.001
gb AF081971.1 AF081971	Vireo cassinii cassinii specimen-vou...	<u>44</u>	0.001
gb AF081970.1 AF081970	Vireo solitarius alticola country US...	<u>44</u>	0.001
gb AF081969.1 AF081969	Vireo solitarius alticola country US...	<u>44</u>	0.001
gb AF081968.1 AF081968	Vireo solitarius alticola country US...	<u>44</u>	0.001
gb AF081967.1 AF081967	Vireo solitarius alticola country US...	<u>44</u>	0.001
gb AF081966.1 AF081966	Vireo solitarius solitarius specimen...	<u>44</u>	0.001
gb AF081965.1 AF081965	Vireo solitarius solitarius specimen...	<u>44</u>	0.001
gb AF081964.1 AF081964	Vireo solitarius solitarius specimen...	<u>44</u>	0.001
gb AF081962.1 AF081962	Vireo flavifrons specimen-voucher LS...	<u>44</u>	0.001
gb AF081961.1 AF081961	Vireo flavifrons specimen-voucher LS...	<u>44</u>	0.001
gb AF081950.1 AF081950	Vireo leucophrys leucophrys specimen...	<u>44</u>	0.001
gb AF081959.1 AF081959	Vireolanius leucotis leucotis cytoch...	<u>44</u>	0.001
gb AF112405.2 AF112405	Barbus anoplus cytochrome b (cytb) g...	<u>44</u>	0.001
gb AF144317.1 AF144317	Amphiprion ocellaris isolate 3 haplo...	<u>44</u>	0.001
gb AF144316.1 AF144316	Amphiprion ocellaris haplotype 3DH11...	<u>44</u>	0.001
gb AF144315.1 AF144315	Amphiprion ocellaris haplotype 3DH15...	<u>44</u>	0.001
gb AF144314.1 AF144314	Amphiprion ocellaris isolate 2 haplo...	<u>44</u>	0.001
gb AF144313.1 AF144313	Amphiprion ocellaris isolate 1 haplo...	<u>44</u>	0.001
gb AF144312.1 AF144312	Amphiprion ocellaris haplotype 3DH12...	<u>44</u>	0.001
gb AF144311.1 AF144311	Amphiprion ocellaris haplotype 3DH1 ...	<u>44</u>	0.001
gb AF144310.1 AF144310	Amphiprion ocellaris isolate 2 haplo...	<u>44</u>	0.001
gb AF144309.1 AF144309	Amphiprion ocellaris isolate 1 haplo...	<u>44</u>	0.001
ref NC_001567.1  Bos taurus mitochondrion, complete genome		<u>44</u>	0.001
gb AF212124.1 AF212124	Anolis schwartzi cytochrome b gene. ...	<u>44</u>	0.001
gb AF182706.1 AF182706	Phapitreron amethystina cytochrome b...	<u>44</u>	0.001
gb AF010406.1 AF010406	Ovis aries complete mitochondrial ge...	<u>44</u>	0.001
gb AF096452.1 AF096452	Platysteira cyanea cytochrome b gene...	<u>44</u>	0.001
gb AF281619.1 AF281619	Elaphe obsoleta LSUMZ39162 cytochrom...	<u>44</u>	0.001
gb AF281618.1 AF281618	Elaphe obsoleta LSUMZ H15896 cytochr...	<u>44</u>	0.001
gb AF281608.1 AF281608	Elaphe obsoleta LSUMZ H14782 cytochr...	<u>44</u>	0.001
gb AF281602.1 AF281602	Elaphe obsoleta LSUMZ H3388 cytochro...	<u>44</u>	0.001
gb AF310069.1 AF310069	Elaenia martinica cytochrome b gene...	<u>44</u>	0.001
gb AF146616.1 AF146616	Actophilornis africanus cytochrome b...	<u>44</u>	0.001
gb AF271410.1 AF271410	Galago moholi cytochrome b (cyt b) g...	<u>44</u>	0.001
gb AF290139.1 AF290139	Peucedramus taeniatus cytochrome b (...)	<u>44</u>	0.001
ref NC_002504.1  Lama pacos mitochondrion, complete genome		<u>44</u>	0.001
gb AF161901.1 AF161901	Microtus ochrogaster cytochrome b ge...	<u>44</u>	0.001
gb AF119253.1 AF119261	Myopus schisticolor cytochrome b gen...	<u>44</u>	0.001
gb AF119259.1 AF119259	Synaptomyia borealis cytochrome b gen...	<u>44</u>	0.001
gb AF288454.1 AF288454	Nyctereutes procyonoides koreensis c...	<u>44</u>	0.001
gb AF153895.1 AF153895	Microtus griseocaudatus cytochrome B (cytB...	<u>44</u>	0.001
gb AF121642.1 AF121642	Machaeropterus regulus acrolatus cy...	<u>44</u>	0.001
gb AF121647.1 AF121647	Machaeropterus pyrocephalus cytochro...	<u>44</u>	0.001
gb AF121645.1 AF121645	Xenoligeia attronitens cytochrome b gen...	<u>44</u>	0.001
gb AF121645.1 AF121645	Pipra fasciicauda cytochrome b gene....	<u>44</u>	0.001
gb AF121614.1 AF121614	Pyroderces scutatus cytochrome b gene...	<u>44</u>	0.001
gb AF121613.1 AF121613	Cephalopterus ornatus cytochrome b g...	<u>44</u>	0.001
gb AF121628.1 AF121628	Turdampelie cryptolephe cytochrome ...	<u>44</u>	0.001
gb AF121631.1 AF121631	Porphyrolaemus porphyrolaemus cytochro...	<u>44</u>	0.001
gb AF121619.1 AF121619	Amphilophus tequendama cytochrome b ge...	<u>44</u>	0.001
gb AF121618.1 AF121618	Alpicola chinolepidota cytochrome b...	<u>44</u>	0.001
gb AF121619.1 AF121619	Rupicola peruviana cytochrome b gene...	<u>44</u>	0.001
gb AF121626.1 AF121626	Dolichonyx oryzivorus cytochrome b gene...	<u>44</u>	0.001

gb AF127201.1 AF127201	Myrmothera campanisona cytochrome b ...	4.4	0.001
gb AF127192.1 AF127192	Grallaria ruficapilla cytochrome b g...	4.4	0.001
gb AF127189.1 AF127189	Grallaria vazia cytochrome b gene, p...	4.4	0.001
gb AF197849.1 AF197849	Sericornis frontalis cytochrome b ge...	4.4	0.001
gb AF197847.1 AF197847	Pardalotus striatus cytochrome b gen...	4.4	0.001
ref NC_000889.1	Hippopotamus amphibius mitochondrion, comp...	4.4	0.001
ref NC_002079.1	Carassius auratus mitochondrion, complete ...	4.4	0.001
ref NC_001794.1	Macropus robustus mitochondrion, complete ...	4.4	0.001
ref NC_001610.1	Didelphis virginiana mitochondrion, comple...	4.4	0.001
gb AF201612.1 AF201612	Stomatorhinus sp. CU79703 cytochrome...	4.4	0.001
gb AF097931.1 AF097931	Amphiprion clarkii cytochrome b gene...	4.4	0.001
gb AF097927.1 AF097927	Amphiprion ocellaris cytochrome b ge...	4.4	0.001
gb J01394.1 BOVMT_Bos	taurus mitochondrion, complete genome	4.4	0.001
gb AF168760.1 AF168760	Apalone spinifera isolate TXsc cytoc...	4.4	0.001
gb AF168759.1 AF168759	Apalone spinifera isolate TXki cytoc...	4.4	0.001
gb AF168758.1 AF168758	Apalone spinifera isolate TXcc cytoc...	4.4	0.001
gb AF168756.1 AF168756	Apalone spinifera isolate NMrg cytoc...	4.4	0.001
gb AF182381.1 AF182381	Petrochelidon rufofumigata isolate E...	4.4	0.001
gb AF182380.1 AF182380	Petrochelidon rufofumigata isolate E...	4.4	0.001
gb U89187.1 MMU89187	Momotus mexicanus cytochrome b (cytb) ...	4.4	0.001
gb AF193833.1 AF193833	Botaurus lentiginosus cytochrome b g...	4.4	0.001
gb AF193822.1 AF193822	Ardea alba cytochrome b gene, partia...	4.4	0.001
gb AF193821.1 AF193821	Ardea herodias cytochrome b gene, pa...	4.4	0.001
gb AF217837.1 AF217837	Paranaja multifasciata cytochrome b ...	4.4	0.001
gb AF217835.1 AF217835	Naja kaouthia cytochrome b gene, com...	4.4	0.001
gb AF217834.1 AF217834	Laticauda colubrina cytochrome b gen...	4.4	0.001
gb AF217831.1 AF217831	Calliophis japonicus cytochrome b ge...	4.4	0.001
gb AF217823.1 AF217823	Micruroides euryxanthus cytochrome b...	4.4	0.001
gb AF217819.1 AF217819	Drysdalia coronata cytochrome b gene...	4.4	0.001
gb AF217815.1 AF217815	Austrelaps superbus cytochrome b gen...	4.4	0.001
gb AF118156.1 AF118156	Terenura humeralis specimen-voucher ...	4.4	0.001
gb AF209938.1 AF209938	Euura atra isolate 62 cytochrome b g...	4.4	0.001
gb AF209933.1 AF209933	Euura atra isolate C cytochrome b ge...	4.4	0.001
gb AF059104.1 AF059104	Marmaronetta angustirostris cytochro...	4.4	0.001
gb AF059102.1 AF059102	Lophonetta specularoides cytochrome ...	4.4	0.001
gb AF059054.1 AF059054	Amazonetta brasiliensis cytochrome b...	4.4	0.001
gb AF192646.1 AF192646	Hippocampus barbouri haplotype PH.22...	4.4	0.001
gb AF192645.1 AF192645	Hippocampus barbouri haplotype PH.13...	4.4	0.001
gb AF160614.1 AF160614	Cricetomys gambianus Cgam518 cytochr...	4.4	0.001
gb AF160613.1 AF160613	Cricetomys emini Cemi511 cytochrome ...	4.4	0.001
gb AF160612.1 AF160612	Cricetomys emini Cemi530 cytochrome ...	4.4	0.001
gb AF160611.1 AF160611	Cricetomys emini Cemi637 cytochrome ...	4.4	0.001
gb AF160610.1 AF160610	Cricetomys emini Cemi636 cytochrome ...	4.4	0.001
gb AF160604.1 AF160604	Calomyscus bailwardi Chals576 cytochr...	4.4	0.001
gb AF160560.1 AF160560	Eliurus majori Emaj642 cytochrome b ...	4.4	0.001
gb AF160559.1 AF160559	Eliurus majori Emaj641 cytochrome b ...	4.4	0.001
gb AF160558.1 AF160558	Eliurus majori Emaj639 cytochrome b ...	4.4	0.001
gb AF160557.1 AF160557	Eliurus majori Emaj638 cytochrome b ...	4.4	0.001
gb AF160555.1 AF160555	Eliurus majori Emaj614 cytochrome b ...	4.4	0.001
gb AF160554.1 AF160554	Eliurus majori Emaj617 cytochrome b ...	4.4	0.001
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gb AF160552.1 AF160552	Eliurus majori Emaj556 cytochrome b ...	4.4	0.001
gb AF160551.1 AF160551	Eliurus majori Emaj561 cytochrome b ...	4.4	0.001
gb AF160550.1 AF160550	Eliurus majori Emaj443 cytochrome b ...	4.4	0.001
gb AF160549.1 AF160549	Eliurus majori Emaj444 cytochrome b ...	4.4	0.001
gb AF016287.1 AF016287	Damaliscus pygargus cytochrome b (cyt...)	4.4	0.001
gb AF016286.1 AF016286	Oryx leucoryx cytochrome b (cytb) ge...	4.4	0.001
gb AF016283.1 AF016283	Antilope cervicapra cytochrome b (cyt...)	4.4	0.001
gb AF016281.1 AF016281	Antidorcas marsupialis cytochrome b ...	4.4	0.001
gb AF016278.1 AF016278	Tragelaphus oryx cytochrome b (cytb) ...	4.4	0.001
gb AF016276.1 AF016276	Tragelaphus euryceros cytochrome b (...	4.4	0.001
gb AF015274.1	Tetracerus quadricornis cytochrome b (cytb) ...	4.4	0.001
ref NC_001941.1	Ovis aries mitochondrion, complete genome	4.4	0.001
gb AF109698.1 AF109698	Microcyzomyia minutus cytochrome B (c...	4.4	0.001
gb AF109697.1 AF109697	Rhipidomys nicei cytochrome B (cytB ...	4.4	0.001
gb AF109671.1 AF109671	Thomomys daphnis cytochrome B (cytB ...	4.4	0.001
gb AF109652.1 AF109652	Scaptoecetes tumidus cytochrome B (cyt...)	4.4	0.001
gb AF012720.1 AF012720	Megamuntiacus vuquengense cytochrom...	4.4	0.001
gb AF012719.1	Muntiacus muntjak cytochrome b gene, mito...	4.4	0.001
gb AF012718.1 AF012718	Scenella coeruleoalba cytochrome b g...	4.4	0.001
gb AF012717.1 AF012717	Scenella coeruleoalba cytochrome b g ...	4.4	0.001
gb AF012716.1 AF012716	Scenella coeruleoalba cytochrome b g ...	4.4	0.001

gb AF084074.1 AF084074	Lagenorhynchus albostriatus cytochrome...	44	0.001
gb AF090750.1 AF090750	Gobio gobio balcanicus cytochrome b ...	44	0.001
gb AF157939.1 AF157939	Spermophilus columbianus columbianus...	44	0.001
gb AF157937.1 AF157937	Spermophilus washingtoni isolate S89...	44	0.001
gb AF157936.1 AF157936	Spermophilus washingtoni isolate S88...	44	0.001
gb AF157915.1 AF157915	Spermophilus richardsoni isolate S63...	44	0.001
gb AF157914.1 AF157914	Spermophilus richardsoni isolate S62...	44	0.001
gb AF157912.1 AF157912	Spermophilus undulatus isolate S60 c...	44	0.001
gb AF157906.1 AF157906	Spermophilus undulatus isolate S55 c...	44	0.001
gb AF157891.1 AF157891	Spermophilus elegans elegans isolate...	44	0.001
gb AF157882.1 AF157882	Spermophilus columbianus columbianus...	44	0.001
gb AF157859.1 AF157859	Spermophilus citellus isolate S118 c...	44	0.001
gb AF157858.1 AF157858	Spermophilus citellus isolate S117 c...	44	0.001
gb AF157839.1 AF157839	Spermophilus elegans elegans isolate...	44	0.001
gb AF030497.1 AF030497	Crocidura brunnea cytochrome b (cyt ...	44	0.001
gb U03541.2 LAU03541	Lenoxus apicalis cytochrome b gene, pa...	44	0.001
gb AF009951.2 AF009951	Heros appendiculatus cytochrome b (c...	44	0.001
gb AF009941.1 AF009941	Tomocichla tuba cytochrome b (cytb) ...	44	0.001
gb AF009925.1 AF009925	Archocentrus sajica cytochrome b (Cy...)	44	0.001
gb AF094633.1 AF094633	Stachyris whiteheadi cytochrome b ge...	44	0.001
gb AF094621.1 AF094621	Eminia lepida cytochrome b gene, par...	44	0.001
gb AF094618.1 AF094618	Hypergerus atriceps cytochrome b gen...	44	0.001
gb AF166348.1 AF166348	Phascolarctos cinereus cytochrome b ...	44	0.001
gb AF158697.1 AF158697	Geomys bursarius ozarkensis cytochro...	44	0.001
gb AF158694.1 AF158694	Geomys bursarius majusculus cytochro...	44	0.001
gb AF158693.1 AF158693	Geomys bursarius bursarius cytochrom...	44	0.001
gb AF158688.1 AF158688	Geomys bursarius missouriensis cytoc...	44	0.001
gb AF100720.1 AF100720	Spermophilus citellus cytochrome b (...)	44	0.001
gb AF091632.1 AF091632	Bubalus depressicornis cytochrome b ...	44	0.001
gb AF102815.1 AF102815	Dromiciops gliroides cytochrome b ge...	44	0.001
gb AF102814.1 AF102814	Vombatus ursinus cytochrome b gene, ...	44	0.001
gb AF022065.1	Tragelaphus euryceros cytochrome b (cytb) ge...	44	0.001
gb AF022059.1	Kobus ellipsiprymnus cytochrome b (cytb) gen...	44	0.001
gb AF022058.1	Antilope cervicapra cytochrome b (cytb) gene...	44	0.001
gb AF022057.1	Tragelaphus oryx cytochrome b (cytb) gene, m...	44	0.001
gb AF022054.1	Antidorcas marsupialis cytochrome b (cytb) g...	44	0.001
gb AF016637.1 AF016637	Connochaetes gnou cytochrome b (cytb) ...	44	0.001
gb U69863.1 PSU69863	Python sebae cytochrome b (cytb) gene....	44	0.001
gb U69844.1 LTU69844	Lichanura trivirgata cytochrome b (cyt ...	44	0.001
gb AF143193.1 AF143193	Epinephelus sp. cytochrome b (cytb) ...	44	0.001
gb AF121222.1 AF121222	Amphiprion ocellaris isolate 8 cytoc...	44	0.001
gb AF096625.1 AF096625	Kobus ellipsiprymnus defassa cytochr...	44	0.001
gb AF096624.1 AF096624	Kobus ellipsiprymnus ellipsiprymnus c...	44	0.001
gb AF081052.1 AF081052	Eulemur rubriventer cytochrome b (Cy...)	44	0.001
gb AF081049.1 AF081049	Eulemur macaco macaco cytochrome b (...)	44	0.001
gb AF081048.1 AF081048	Eulemur fulvus albifrons cytochrome ...	44	0.001
gb AF082063.1 AF082063	Elminia longicauda cytochrome b gene...	44	0.001
emb AJ010957.1 HAAJ10957	Hippopotamus amphibius complete mi...	44	0.001
gb U76506.1 CLU76506	Chlamydera lauterbachii cytochrome b g...	44	0.001
gb U76504.1 CCU76504	Chlamydera cerviniventris cytochrome b...	44	0.001
gb U75505.1 ASUT75505	Amblyornis subalaris cytochrome b gene...	44	0.001
gb U76503.1 APU76503	Archboldia papuensis cytochrome b gene...	44	0.001
gb U76508.1 AIU76508	Amblyornis inornatus cytochrome b gene...	44	0.001
gb AF014969.1 AF014969	Connochaetes taurinus cytochrome b g...	44	0.001
gb AF051875.1 AF051875	Rhodeus ocellatus cytochrome b (cytb...)	44	0.001
gb AF082007.1 AF082007	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082005.1 AF082005	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082005.1 AF082005	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082004.1 AF082004	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082003.1 AF082003	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082002.1 AF082002	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082001.1 AF082001	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082000.1 AF082000	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081999.1 AF081999	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081999.1 AF081999	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081997.1 AF081997	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081996.1 AF081996	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081995.1 AF081995	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081994.1 AF081994	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081993.1 AF081993	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF081992.1 AF081992	Vireo plumbeus plumbeus specimen-vou...	44	0.001

gb AF081991.1 AF081991	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb S73150.1 S73150	cytochrome b ( <i>Spermophilus richardsoni</i> )...	44	0.001
gb AF012235.1 AF012235	Cryptomys hottentotus natalensis cyt...	44	0.001
gb US3580.1 NCUS3580	<i>Nycticebus coucang</i> cytochrome b (cyt b...)	44	0.001
gb US3577.1 EFUS3577	<i>Eulemur fulvus rufus</i> cytochrome b (cyt...)	44	0.001
gb US3576.1 EFUS3576	<i>Eulemur fulvus collaris</i> cytochrome b (...)	44	0.001
gb U95512.1 ESERCYTB2	<i>Eptesicus serotinus</i> 3' cytochrome b (...)	44	0.001
gb U95508.1 PKUHLCYTB2	<i>Pipistrellus kuhli</i> 5' cytochrome b (...)	44	0.001
gb U17868.1 BTU17868	<i>Budorcas taxicolor taxicolor</i> cytochrom...	44	0.001
gb U17867.1 BTU17867	<i>Budorcas taxicolor bedfordi</i> cytochrome...	44	0.001
gb U17860.1 ODU17860	<i>Ovis dalli</i> cytochrome b gene, mitochon...	44	0.001
gb U17859.1 OCU17859	<i>Ovis canadensis</i> cytochrome b gene, mit...	44	0.001
emb AJ010556.1 ASPO10556	<i>Acomys spinosissimus</i> mitochondrial...	44	0.001
gb AF034736.1 AF034736	<i>Capra falconeri</i> cytochrome b (cytb) ...	44	0.001
gb AF034730.1 AF034730	<i>Ovis aries</i> cytochrome b (cytb) gene, ...	44	0.001
gb AF034729.1 AF034729	<i>Ovis vignei</i> cytochrome b (cytb) gene...	44	0.001
gb AF034728.1	<i>Ovis dalli dalli</i> cytochrome b (cytb) gene, m...	44	0.001
gb AF034727.1	<i>Ovis ammon darwini</i> cytochrome b (cytb) gene, ...	44	0.001
gb AF034724.1 AF034724	<i>Pantholops hodgsonii</i> cytochrome b (cy...)	44	0.001
gb AF034722.1 AF034722	<i>Addax nasomaculatus</i> cytochrome b (cy...)	44	0.001
gb U72038.1 MMU72038	<i>Monodon monoceros</i> cytochrome b (cytb), ...	44	0.001
gb U72037.1 DLUT72037	<i>Delphinapterus leucas</i> cytochrome b (cy...)	44	0.001
gb M99455.1 MUMXMTCYTB	<i>Murexia longicaudata</i> cytochrome b gen...	44	0.001
gb L29055.1 SHPMTIDLOOP	Sheep mitochondrial cytochrome b (Cy...)	44	0.001
gb AF082047.1 AF082047	<i>Coccyzus americanus</i> cytochrome b gen...	44	0.001
gb AF038286.1 AF038286	<i>Antechinus minimus</i> cytochrome b gene...	44	0.001
gb AF038284.1 AF038284	<i>Antechinus swainsonii</i> cytochrome b g...	44	0.001
gb AF059093.1 AF059093	<i>Anas undulata</i> cytochrome b gene, par...	44	0.001
gb AF059092.1 AF059092	<i>Anas superciliosa rogersi</i> cytochrome...	44	0.001
gb AF059091.1 AF059091	<i>Anas sparsa</i> cytochrome b gene, parti...	44	0.001
gb AF059080.1 AF059080	<i>Anas melleri</i> cytochrome b gene, part...	44	0.001
gb AF059078.1 AF059078	<i>Anas laysanensis</i> cytochrome b gene, ...	44	0.001
gb AF052240.1 AF052240	<i>Anairetes flavirostris</i> cytochrome b ...	44	0.001
gb AF006240.1 AF006240	<i>Mitospingus cassini</i> cytochrome b (...)	44	0.001
gb AF006227.1 AF006227	<i>Dacnis cayana</i> cytochrome b (cytb) ge...	44	0.001
gb AF047447.1 AF047447	<i>Oryx leucoryx</i> cytochrome b gene, mit...	44	0.001
gb U07576.1 AHU07576	<i>Antechinus habbema</i> mitochondrial cytoc...	44	0.001
gb AF028180.1 AF028180	<i>Urocyon cinereoarctatus</i> cytochrome ...	44	0.001
gb AF028178.1 AF028178	<i>Pseudalopex sechurae</i> cytochrome b (c...	44	0.001
gb AF028170.1 AF028170	<i>Vulpes zerda</i> cytochrome b (cytb) gen...	44	0.001
gb M99454.1 ASWMTSCYTB	<i>Antechinus stuartii</i> cytochrome b gen...	44	0.001
gb M99453.1 ASWMTCYTB	<i>Antechinus swainsonii</i> cytochrome b ge...	44	0.001
gb U23461.1 ANU23461	<i>Antechinus naso</i> cytochrome b gene, mit...	44	0.001
gb U87138.1 TVU87138	<i>Trichosurus vulpecula</i> cytochrome b (cy...)	44	0.001
gb U07590.1 PMU07590	<i>Planigale maculata</i> mitochondrial cytoc...	44	0.001
emb AJ004326.1 PTAJ4326	<i>Phylloscopus trochilus</i> mitochondria...	44	0.001
gb AF020255.1 AF020255	<i>Cyclura nubila</i> cytochrome b (cytb) g...	44	0.001
emb Y19184.1 LPA19184	Lama pacos complete mitochondrial genome	44	0.001
gb U88862.1 Amphilophus	<i>citrinellum</i> cytochrome b (cytb) ge...	44	0.001
gb U88859.1 Thorichthys	<i>aureum</i> cytochrome b (cytb) gene, m...	44	0.001
gb U88858.1 Thorichthys	<i>cf. aureum</i> cytochrome b (cytb) gen...	44	0.001
gb U88857.1 Kerichthys	<i>labridens</i> cytochrome b (cytb) gene....	44	0.001
gb U88856.1 Kerichthys	<i>carpintis</i> cytochrome b (cytb) gene, ...	44	0.001
emb Y10524.1 MIMRGEN	<i>Macropus robustus</i> complete mitochondrial...	44	0.001
gb U811357.1 CSU811357	<i>Chelydra serpentina</i> cytochrome b gene...	44	0.001
gb U811356.1 CLU811356	<i>Chelodina longicollis</i> cytochrome b gen...	44	0.001
gb U75354.1 LUU75354	<i>Leptomyrmex unicolor</i> cytochrome b gene...	44	0.001
gb U77332.1 GCU77332	<i>Gymnothrinus cyanocephala</i> cytochrome-b ...	44	0.001
emb Z229573.1 OVMTCGNME	<i>Didelphis virginiana</i> complete mitoch...	44	0.001
emb AJ222679.1 BTCYTOS	<i>Boselaphus tragocamelus</i> mitochondria...	44	0.001
emb AJ222680.1 TSCYTOS	<i>Tragelaphus spekii</i> mitochondrial cyt...	44	0.001
emb AJ222689.1 ODCTOB	<i>Oryx dammah</i> mitochondrial cytochrome...	44	0.001
gb M29466.1 PMLMTCYTB	<i>Parameles nasuta</i> cytochrome b gene, c...	44	0.001
gb M99453.1 THNMTCYTB	<i>Thylacinus cynocephalus</i> cytochrome b...	44	0.001
gb M29450.1 DAVMTCYTB	<i>Oasyurus hallucatus</i> cytochrome b gene...	44	0.001
gb U29717.1 PMU29717	<i>Paradiseaea minor</i> cytochrome b gene, mi...	44	0.001
gb U15201.1 PRU15201	<i>Paradiseaea rudolphi</i> mitochondrial cyto...	44	0.001
gb U15203.1 EAU15203	<i>Eglinachus albisetosus</i> mitochondrial cyt...	44	0.001
gb U15200.1 DRU15200	<i>Diphyllodes reproductus</i> mitochondrial c...	44	0.001
emb AJ999474.1 STA1474	<i>Sorex tundrensis</i> partial mitochondrial...	44	0.001
emb AJ999471.1 STA1471	<i>Sorex tundrensis</i> partial mitochondrial...	44	0.001

emb AJ000438.1 SIAJ438	Sorex isodon partial mitochondrial c...	44	0.001
emb AJ000437.1 SIAJ437	Sorex isodon partial mitochondrial c...	44	0.001
emb AJ000428.1 SAAJ428	Sorex arcticus partial mitochondrial...	44	0.001
emb AJ000427.1 SAAJ427	Sorex arcticus ssp. maritimensis par...	44	0.001
emb AJ000426.1 SAAJ426	Sorex asper partial mitochondrial cy...	44	0.001
emb AJ000425.1 SAAJ425	Sorex asper partial mitochondrial cy...	44	0.001
emb AJ000418.1 SGAJ418	Sorex granarius partial mitochondria...	44	0.001
emb AJ000417.1 SGAJ417	Sorex granarius partial mitochondria...	44	0.001
emb AJ000416.1 SAAJ416	Sorex araneus partial mitochondrial ...	44	0.001
emb AJ004793.1 HCAJ4793	Hippolais caligata ssp. caligata mi...	44	0.001
emb AJ004792.1 HCAJ4792	Hippolais caligata ssp. rama mitoch...	44	0.001
gb U15718.1 RSUL5718	Ramphocelus sanguinolentus cytochrome ...	44	0.001
gb L11905.1 CGYMTCYTB0	Cratogeomys gymnurus mitochondrial c...	44	0.001
gb U34679.1 POU34679	Philander opossum cytochrome b light s...	44	0.001
gb L11907.1 CGYMTCYTB0	Cratogeomys goldmani rubellus mitoch...	44	0.001
gb L11906.1 CGYMTCYTB0	Cratogeomys merriami mitochondrial c...	44	0.001
gb L11902.1 CGYMTCYTB0	Cratogeomys castanops castanops mito...	44	0.001
emb X92524.1 SLCYTB	S.longirostris cytochrome b gene (compl...	44	0.001
gb U46771.1 ACU46771	Anthus campestris cytochrome b gene, m...	44	0.001
dbi AB021773.1 AB021773	Anguilla interioris mitochondrial c...	44	0.001
dbi AB006953.1 AB006953	Carassius auratus langsdorfi mitoch...	44	0.001
emb Z73492.1 MTPTRCYTB	P.trochilus mitochondrial cytochrome...	44	0.001
dbi AB035239.1 AB035239	Osteoglossum farrerai mitochondria...	44	0.001
emb X92532.1 MMCYTB2	M.monoceros cytochrome b gene (complet...	44	0.001
emb X74260.1 MIVOCYTB	V.olivaceus mitochondrion gene for cy...	44	0.001
emb X56293.1 MISLCYTB0	S.longirostris mitochondrion cyt b gen...	44	0.001
emb X56292.1 MISLCYTB0	S.longirostris mitochondrion cyt b ge...	44	0.001
emb X74256.1 MIPVVCYTB	P.violaceus mitochondrion gene for cy...	44	0.001
emb X82304.1 MIPHVCYTB0	P.hispida mitochondrial cytochrome b...	44	0.001
emb X82302.1 MIPFCYTB0	P.fasciata mitochondrial cytochrome ...	44	0.001
emb X56284.1 MIOACYTB	O.aries mitochondrion cyt b gene for c...	44	0.001
emb X74252.1 MIMKCYTB	M.keraudrenii mitochondrion gene for ...	44	0.001
emb X72005.1 MILWCYTB	L.weddelli mitochondrial gene for cyt...	44	0.001
emb X74259.1 MILLCYTB	L.ludovicianus mitochondrion gene for...	44	0.001
emb Y08814.1 MIHLCYTB0	H.liberiensis mitochondrial cytochro...	44	0.001
emb Y08813.1 MIHACYTB	H.amphibius mitochondrial cytochrome ...	44	0.001
emb X56287.1 MIGCCYTB	G.camelopardalis mitochondrion cyt b...	44	0.001
emb X74253.1 MIEFCYTB	E.fastuosus mitochondrion gene for cy...	44	0.001
emb X60941.1 MIZACB33	Epimachus albertisi mitochondrial ge...	44	0.001
emb X74255.1 MIDMCYTB	D.magnificus mitochondrion gene for c...	44	0.001
emb X56289.1 MICHCCYTB	C.hircus mitochondrion cyt b gene for ...	44	0.001
emb V00654.1 MIBTXX	Bos taurus complete mitochondrial genome	44	0.001
emb X50940.1 MIAMCB33	A.macgregoriae mitochondrial gene for...	44	0.001
emb X92530.1 LACYTB	L.albirostris cytochrome b gene (comple...	44	0.001
gb U09265.1 CAU09265	Coccyzus americanus mitochondrion cyto...	44	0.001
dbi AB023906.1 AB023906	Petaurista leucogenys mitochondrial...	44	0.001
dbi AB023905.1 AB023905	Petaurista leucogenys mitochondrial...	44	0.001
dbi AB023904.1 AB023904	Petaurista leucogenys mitochondrial...	44	0.001
dbi AB023903.1 AB023903	Petaurista leucogenys mitochondrial...	44	0.001
dbi D88983.1 D88983	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbi D88638.1 D88638	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbi D88636.1 D88636	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbi D88635.1 D88635	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbi D88633.1 D88633	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbi D88632.1 D88632	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbi D88630.1 D88630	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbi D88628.1 D88628	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbi D88627.1 D88627	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbi D84204.1 GOTMTCB0	Capra aegagrus mitochondrial DNA for ...	44	0.001
dbi D84202.1 GOTMTCB0	Capra falconeri mitochondrial DNA for ...	44	0.001
dbi D82893.1 D82893	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbi D82892.1 D82892	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbi D82899.1 D82899	Bos javanicus mitochondrial DNA for cyt...	44	0.001
dbi D21212.1 BBUMTCB0	Bubalus arnee bubalis mitochondrial ...	44	0.001
dbi D14537.1 BBUMTCB0	Bubalus bubalis mitochondrial gene for...	44	0.001
dbi A802474.1 A802474	Capra hircus mitochondrial DNA for c...	44	0.001
dbi A8004973.1 A8004973	Capra hircus mitochondrial DNA for c...	44	0.001
dbi A8004971.1 A8004971	Capra hircus mitochondrial DNA for c...	44	0.001
dbi A8004952.1 A8004952	Capra aegagrus mitochondrial DNA for c...	44	0.001
dbi D99549.1 D99549	Anoa depressicornis mitochondrial DNA for...	44	0.001
dbi D99551.1 D99551	Bubalus bubalis mitochondrial DNA for c...	44	0.001

dbj D88634.1 D88634	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj D88631.1 D88631	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj D88629.1 D88629	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj D84205.1 SHPMCBE	Sheep mitochondrial DNA for cytochrom...	44	0.001
dbj D84203.1 SHPMCBC	Ovis musimon mitochondrial DNA for cy...	44	0.001
dbj D84201.1 GOTMTCA	Goat mitochondrial DNA for cytochrome...	44	0.001
dbj D82894.1 D82894	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj D82891.1 D82891	Bubalus quarlesi mitochondrial DNA for ...	44	0.001
dbj D34638.1 BBUMTCBB	Bubalus bubalis mitochondrial gene fo...	44	0.001
dbj D34636.1 BOVMTCBB	Bos javanicus mitochondrial gene for ...	44	0.001
dbj AB037602.1 AB037602	Talpa altaica mitochondrial cytb ge...	44	0.001
dbj AB018985.1 AB018985	Cichlasoma citrinellum mitochondria...	44	0.001
dbj AB004075.1 AB004075	Capra hircus mitochondrial DNA for ...	44	0.001
dbj AB004073.1 AB004073	Capra hircus mitochondrial DNA for ...	44	0.001
dbj AB004070.1 AB004070	Capra hircus mitochondrial DNA for ...	44	0.001
emb X92531.1 DLCYTB	D.leucas cytochrome b gene (complete se...	44	0.001
gb U07565.1 HAU07565	Hippopotamus amphibius mitochondrion c...	44	0.001
gb U10367.1 PVU10367	Ptilonorhynchus violaceus mitochondrio...	44	0.001
gb U10364.1 CMU10364	Chlamydera maculata mitochondrion cyto...	44	0.001
emb Z96068.1 ASZ96068	Acomys spinosissimus DNA for mitochon...	42	0.005
gb U76507.1 AIU76507	Amblyornis inornatus cytochrome b gene...	40	0.021
gb AF157466.1 AF157466	Lepus timidus cytochrome b (Cyb) gen...	40	0.021
gb AF157464.1 AF157464	Lepus corsicanus haplotype 1 cytochr...	40	0.021
gb AF157463.1 AF157463	Lepus corsicanus haplotype 3 cytochr...	40	0.021
gb AY016019.1 AY016018S3	Mullerornis agilis cytochrome b ge...	40	0.021
gb AF027330.1	Akodon olivaceus canescens museum catalog nu...	40	0.021
gb AF027329.1	Akodon olivaceus canescens museum catalog nu...	40	0.021
gb AF027328.1	Akodon olivaceus canescens museum catalog nu...	40	0.021
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gb AF027324.1	Akodon olivaceus canescens museum catalog nu...	40	0.021
gb AF027323.1	Akodon olivaceus canescens museum catalog nu...	40	0.021
gb AF027322.1	Akodon olivaceus beatus museum catalog numbe...	40	0.021
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gb AF027311.1	Akodon olivaceus brachiotis museum catalog n...	40	0.021
gb AF027310.1	Akodon olivaceus brachiotis museum catalog n...	40	0.021
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gb AF027307.1	Akodon olivaceus brachiotis museum catalog n...	40	0.021
gb AF266188.1 AF266188	Gillichthys mirabilis cytochrome b m...	40	0.021
gb AF324034.1 AF324034	Phyllobates aurotaenia isolate Quebr...	40	0.021
gb AF272639.1 AF272639	Clethrionomys gapperi specimen-vouch...	40	0.021
gb AF272636.1 AF272636	Clethrionomys gapperi specimen-vouch...	40	0.021
gb AF272634.1 AF272634	Clethrionomys gapperi specimen-vouch...	40	0.021
gb AF272633.1 AF272633	Clethrionomys gapperi specimen-vouch...	40	0.021
gb AF182711.1 AF182711	Geopelia cuneata cytochrome b gene. p...	40	0.021
gb AF182687.1 AF182687	Columbina picui cytochrome b gene. p...	40	0.021
gb AF155422.1 AF155422	Sigmadon ochrognathus cytochrome b (...	40	0.021
gb AF155400.1 AF155400	Peromyscus pectoralis lacertanus cyto...	40	0.021
gb AF155395.1 AF155395	Peromyscus attwateri isolate 1b cyto...	40	0.021
gb AF155394.1 AF155394	Peromyscus attwateri isolate 1a cyto...	40	0.021
gb AF155392.1 AF155392	Sigmadon ochrognathus isolate ArizAC...	40	0.021
gb AF155391.1 AF155391	Sigmadon ochrognathus isolate McDiv7...	40	0.021
gb AF155390.1 AF155390	Sigmadon ochrognathus isolate Duran4...	40	0.021
gb AF155389.1 AF155389	Sigmadon ochrognathus isolate EleMt8...	40	0.021
gb AF155388.1 AF155388	Sigmadon ochrognathus isolate BbEnd4...	40	0.021
gb AF122521.1 AF122521	Trachypodus dorsalis cytochrome b ...	40	0.021
gb AF266947.1 AF266947	Ureus opalus cytochrome b gene. co...	40	0.021
gb AF205533.1 AF205533	Podarcis sicula cytochrome b gene. p...	40	0.021
gb AF122705.1 AF122705	Kleppocampus rostratus haplotype PK.14...	40	0.021
gb MC_999991.1 Cavia porcellus complex mitochondrial genome	Cavia porcellus complex mitochondrial genome	40	0.021

<u>gb AF004572.1 AF004572</u>	Arvicantis niloticus cytochrome b (...)	<u>40</u>	<u>0.021</u>
<u>gb AF088932.1 AF088932</u>	Sminthopsis psammophila cytochrome b...	<u>40</u>	<u>0.021</u>
<u>gb U62697.1 ORUCYTB2</u>	Oreopholus ruficollis cytochrome b (cy...	<u>40</u>	<u>0.021</u>
<u>gb U62681.1 CACYTB2</u>	Charadrius australis cytochrome b (cyt ...	<u>40</u>	<u>0.021</u>
<u>gb U62707.1 CVERCYTB2</u>	Charadrius veredus cytochrome b (cytb...)	<u>38</u>	<u>0.084</u>
<u>emb AJ004315.1 HCAJ4315</u>	Hippolais caligata mitochondrial cy...	<u>38</u>	<u>0.084</u>

## Alignments

tmpseq_0	1	cctccctagttgttagggattgatcg	26
<u>AF189111</u>	797	.....	772
<u>U86834</u>	858	.....	833
<u>AF123633</u>	56	.....	31
<u>AF123617</u>	104	.....	79
<u>AF127202</u>	107	.....	82
<u>AF127194</u>	107	.....	82
<u>AF217828</u>	845	.....	820
<u>AF160578</u>	869	.....	844
<u>AF009931</u>	869	.....	844
<u>AF091629</u>	869	.....	844
<u>AF034967</u>	869	.....	844
<u>AF038290</u>	869	.....	844
<u>U07577</u>	869	.....	844
<u>U81343</u>	.791	.....	766
<u>AJ222681</u>	869	.....	844
<u>M99464</u>	869	.....	844
<u>AJ225116</u>	869	.....	844
<u>U25738</u>	872	.....	847
<u>U25736</u>	872	.....	847
<u>U15202</u>	872	.....	847
<u>U15204</u>	872	.....	844
<u>X56290</u>	869	.....	844
<u>X56286</u>	869	.....	844
<u>D88639</u>	869	.....	844
<u>D82890</u>	869	.....	844
<u>AFL19261</u>	869	.....	847
<u>AF123615</u>	101	.....	79
<u>AF160603</u>	866	.....	844
<u>U62687</u>	179	.....	157
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<u>D34638</u>	869	.....a.....	844
<u>D34636</u>	869	.....g.....	844
<u>AB037602</u>	869	.....a.....	844
<u>AB018985</u>	869	.....a.....	844
<u>A8004075</u>	869	.....g.....	844
<u>A8004073</u>	869	.....g.....	844
<u>A8004070</u>	869	.....g.....	844
<u>X92531</u>	869	.....g.....	844
<u>U07565</u>	869	.....g.....	844
<u>U10367</u>	773	.....g.....	748
<u>U10364</u>	773	.....g.....	748
<u>Z96068</u>	869	.....g.....	844
<u>U76507</u>	773	.....t.....	749
<u>AF157466</u>	791		772
<u>AF157464</u>	793		774
<u>AF157463</u>	793		774
<u>AY016019</u>	93		74
<u>AF027330</u>	869		850
<u>AF027329</u>	869		850
<u>AF027328</u>	869		850
<u>AF027327</u>	869		850
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<u>AF027314</u>	869		850
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<u>AF027311</u>	869		850
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<u>AF027309</u>	869		850
<u>AF027308</u>	869		850
<u>AF027307</u>	869		850
<u>AF266188</u>	371		352
<u>AF124034</u>	408		389
<u>AF272619</u>	869		850
<u>AF272616</u>	869		850
<u>AF272614</u>	869		850
<u>AF272611</u>	869		850
<u>AF182711</u>	712		693
<u>AF182697</u>	774		755
<u>AF155421</u>	869		850
<u>AF155409</u>	869		850
<u>AF155395</u>	869		850
<u>AF155384</u>	869		850
<u>AF155372</u>	869		850
<u>AF155371</u>	869		850
<u>AF155370</u>	869		850

<u>AF155583</u>	869	.....	850
<u>AF155588</u>	869	.....	850
<u>AF121531</u>	771	.....	752
<u>AF264047</u>	869	.....	850
<u>AF206531</u>	771	.....	752
<u>AF192706</u>	863	.....	844
<u>NC_000884</u>	15032	.....	15013
<u>AF004572</u>	869	.....	850
<u>AF088932</u>	869	.....	850
<u>U62697</u>	176	.....	157
<u>U62681</u>	179	.....	160
<u>U62707</u>	179	.....	154
<u>AJ004315</u>	773	.....	748

Database: nt

Posted date: Mar 2, 2001 12:20 AM

Number of letters in database: 2,863,827,885

Number of sequences in database: 807,597

Lambda K H  
1.37 0.711 1.31

Gapped

Lambda K H  
1.37 0.711 1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 19068

Number of Sequences: 807597

Number of extensions: 19068

Number of successful extensions: 7580

Number of sequences better than 10.0: 2441

length of query: 26

length of database: 2,863,827,885

effective HSP length: 17

effective length of query: 9

effective length of database: 2,850,098,736

effective search space: 25650888624

effective search space used: 25650888624

T: 0

A: 30

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 16 (32.2 bits)

**Table 12.** The other animals belonging to distantly related species analyzed by our primers to demonstrate its universal nature

SN.	Name of the animal
1.	Indian black buck no.1
2.	Indian black buck no 2
3	sheep
4	pig
5	dog
6	chimpanzee (chimss)
7	human (humsk)
8	Hamster
9	crocodile no1
10	crocodile no2
11	turtle no1
12	turtle no2
13	mouse
14	varanus
15	Naga-naga snake
16	Indian elephant
17	hen
18	dugong
19	lizard
20	weaver bird no 1
21	weaver bird no2
22	buffalo no 1
23	buffalo no 2

**CLAIMS**

1 Universal primers named as 'mcb 398' and 'mcb 869' capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level, said primers, having the sequences:

primers name	Sequence (5'-3')
mcb 398	"TACCATGAGGACAAATATCATTCTG"
mcb 869	"CCTCCTAGTTGTTAGGGATTGATCG

2. Primers as claimed in claim 1 wherein the fragment of mitochondrial cytochrome b gene is capable of significantly discriminating amongst various evolutionary lineages of different animal species.

3. Primers as claimed in claim 1 wherein the fragment of mitochondrial cytochrome b gene is flanked by the highly conserved sequences amongst a vast range of animal species.

4. Primers as claimed in claim 1 wherein the fragment on mitochondrial cytochrome b gene which is polymorphic inter-specifically, but monomorphic at intra species sources.

5. Primers as claimed in claim 1 wherein in *Antilope cervicapra* species, the sequences of the fragment mentioned under claim 1 are as follows:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*:  
"taccatgaggacaaatatctttgaggagcaacagtcatcaccaatctccatcgcaatcccatacatcggtacaaacctagtagaatgaatctgaggagggtctcagtagataaagcaacccttacccgattttcgccctccactttatcccccatttatcattgcagcccttaccatagtagcacactgttctccacgaaacaggatccaacaacccacaggaatctcatcagacgcagacaaaatcccatccacccctactacactatcaaagatatcctaggagctctactattaatttaaccctcatgctctagtcctatttcaccggacactgcttgagacccagacaactatacaccagcaaaccctacttaatacacccccacatatcaagcccgaatgatacttcctatttgatacgcaatctccgatcaattctaacaactaggagg"

6. A method for the identification of the animal from a biological sample, said method comprising the steps of:

- isolating and amplifying the DNA from the biological sample to be tested using the primers as claimed in claim 1,
- sequencing the amplified products,
- blasting the sequence resolved in step (b) against mito database of National Centre for Biotechnology Information (NCBI) using BLAST program and determining the most likely family of the animal source of the biological sample.

d) blasting the sequence resolved in step (b) against non-redundant (nr) database of National Centre for Biotechnology Information (NCBI) using BLAST program and determining the most likely genus, species or more precisely the sub-species of the animal source of the biological sample,

5 e) identifying the most significant alignment of the sequence resolved with cytochrome b gene sequence of the animal identified in steps (c) and (d) respectively and selection of these animals as 'reference animals' for further studies,

10 f) isolating and amplifying and sequencing the DNA sequences from the reference animal on both strands in triplicate using the primers as claimed in claim 1,

g) aligning the sequences obtained using CLUSTRAL program and identifying the variable sites amongst the animals analyzed,

15 h) comparing the nucleotide sequences pair-wise to determine the variation among the animals resolved and identifying the nucleotide sequence to which the DNA sequence of the biological sample bears maximum similarity as the source animal of the biological sample.

7. A method as claimed in claim 6 wherein the universal PCR protocol works universally with the DNA template of any unknown animal origin and the universal primers mentioned under column 4.

20 8. A method as claimed in claim 6 wherein the Amplification reactions should be carried out in 20 µl reaction volume containing approximately 20 ng of template DNA, 100µm each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl<sub>2</sub>, 0.5 unit of AmpliTaq Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed should be: an initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35<sup>th</sup> cycles should be held for 10 min.

25 9. A method as claimed in claim 6 wherein the method enables identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.

10. A method as claimed in claim 6 wherein the method is used for animal identification to establish the crime with the criminal beyond a reasonably doubt.

11. A method as claimed in claim 6 wherein the method is used to establish the identity of

biological materials such as skin, horns etc confiscated from animal poachers, if it is that of an endangered species.

12. A method as claimed in claim 6 wherein the method is used for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation of the wildlife resources could be controlled.
- 5 13. A method as claimed in claim 6 wherein the method is used to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented.
- 10 14. A method as claimed in claim 6 wherein the method is used for animal identification to detect the adulteration of animal meat in food products for the purpose of food fortification, by the food fortification agencies.
- 15 15. A method as claimed in claim 6 wherein the method is used to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as if criminals have wontedly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic scientists with human blood.
- 20 16. A method as claimed in claim 6 wherein the method is used so that it can be converted to a (a) COMMERCIAL 'MOLECUALR KIT' and (b) 'DNA CHIPS' based applications for wildlife identification in forensics.

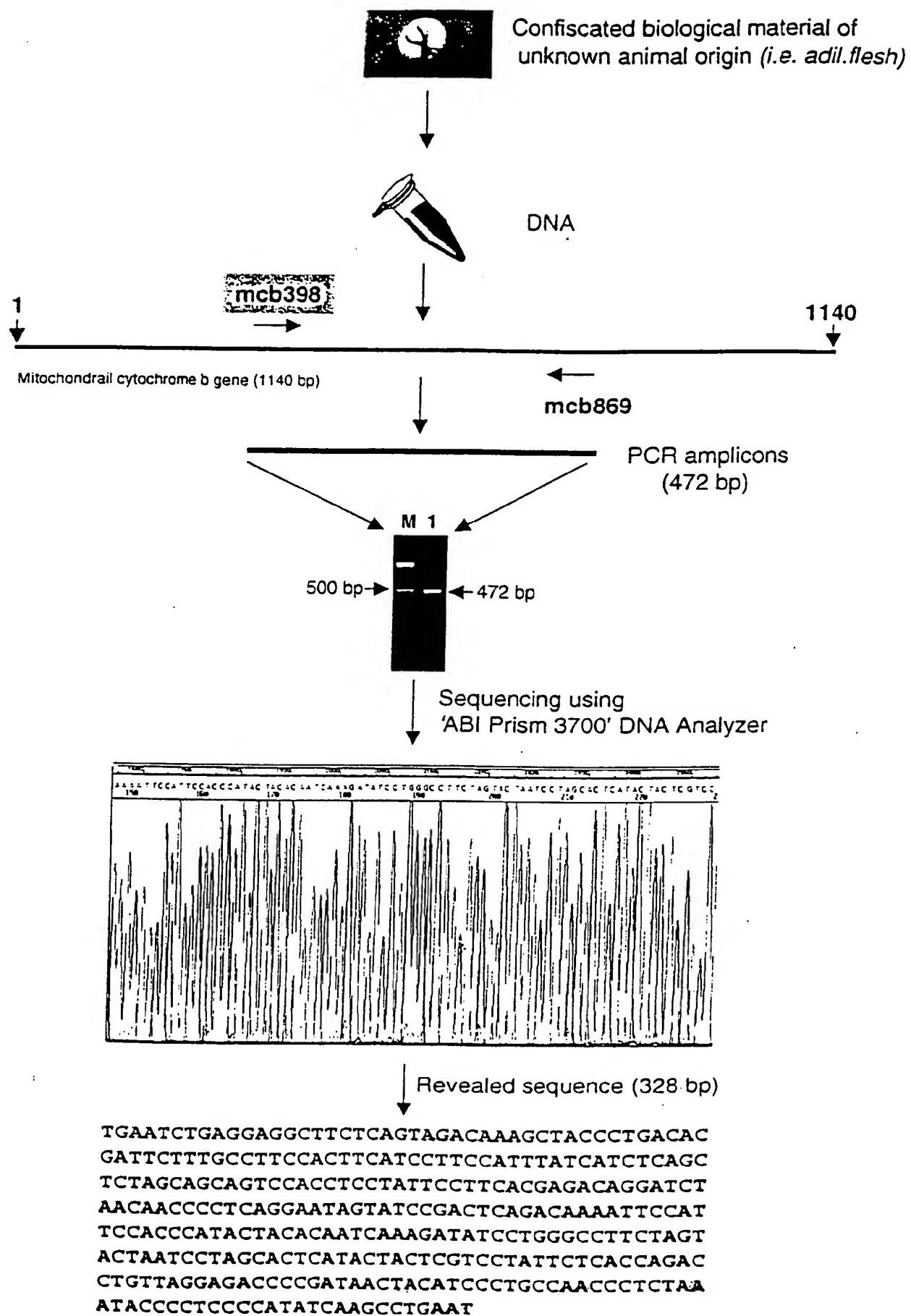
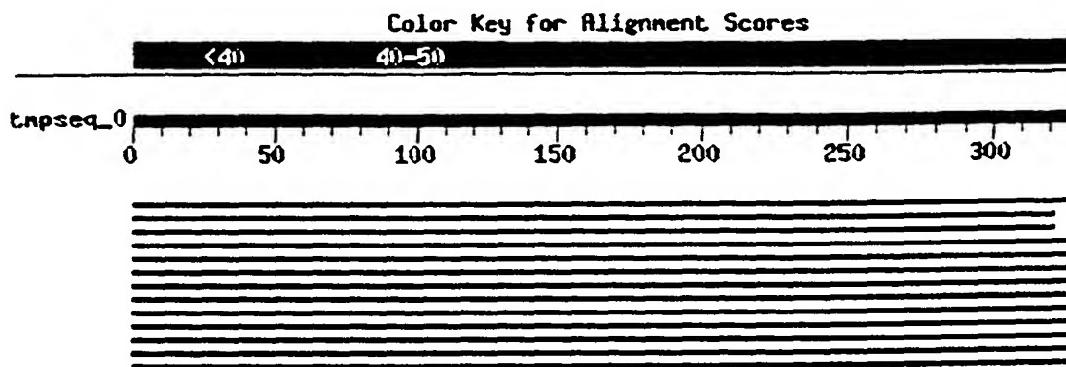


Figure 1 a

Sequence of cytochrome b gene (328 bp) revealed from biological material of unknown origin i.e. '*adil.flesh*' using primers 'mcb398' and 'mcb869'

## Homology search in 'nr' database using 'BLAST'

<http://www.ncbi.nlm.nih.gov/BLAST/>



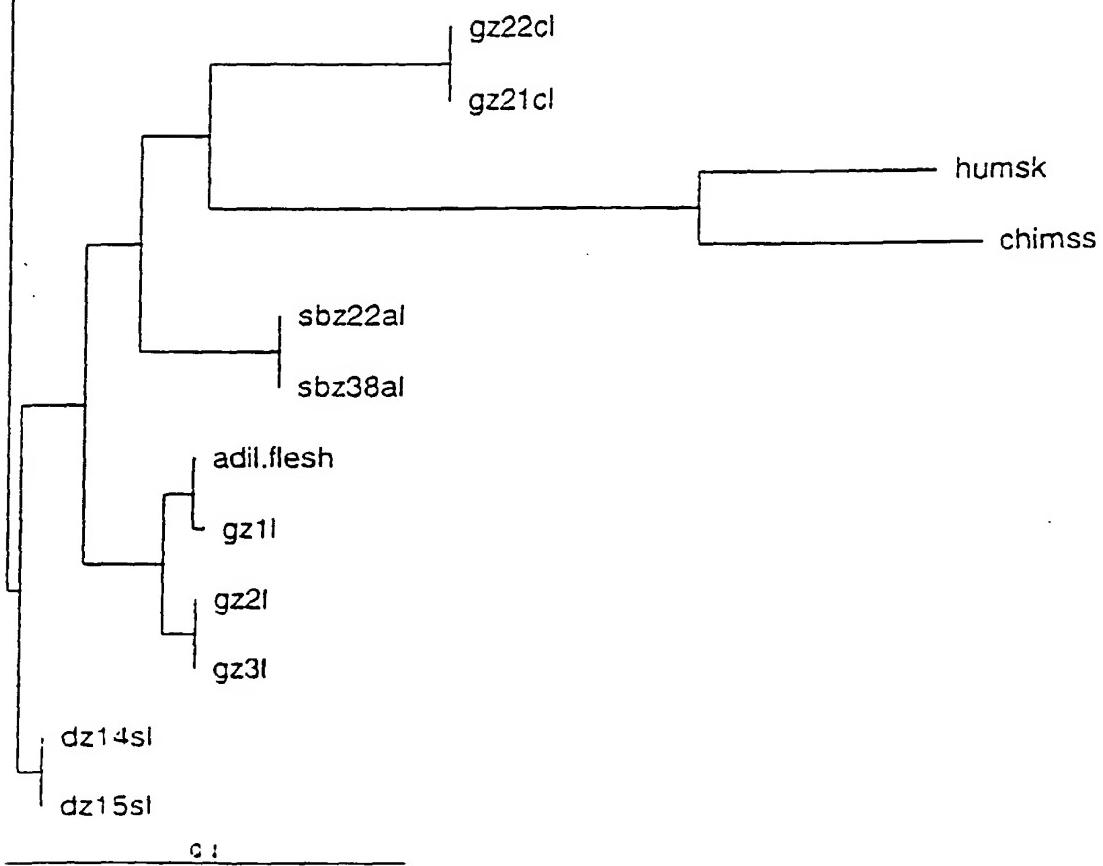
Sequences producing significant alignments:	Score (bits)	E Value
gb AY005809.1  <i>Panthera pardus</i> cytochrome b gene, partial c...	603	e-170
gb AF053054.1 AF053054 <i>Panthera tigris sumatræ</i> isolate Su1...	527	e-147
gb AF053053.1 AF053053 <i>Panthera tigris tigris</i> isolate B7 mi...	527	e-147
gb AF053050.1 AF053050 <i>Panthera tigris corbetti</i> isolate C2 ...	476	e-132
gb AF053049.1 AF053049 <i>Panthera tigris corbetti</i> isolate C1 ...	476	e-132

Selection of reference animals based on above information and further analysis using primers 'mcb398' and 'mcb869'

## Multiple sequence alignments using 'Autoassembler'

**Figure 1 b**

bhz25t NJ-tree showing clustering of 'adil.flesh' with  
'gz1L' i.e.the known normal leopard (*Panthera pardus*)  
bhz26t  
bhz30t  
bhz45t  
bhz56t  
bhz20wt  
bhz23wt  
bhz22wt



**Figure 1c**

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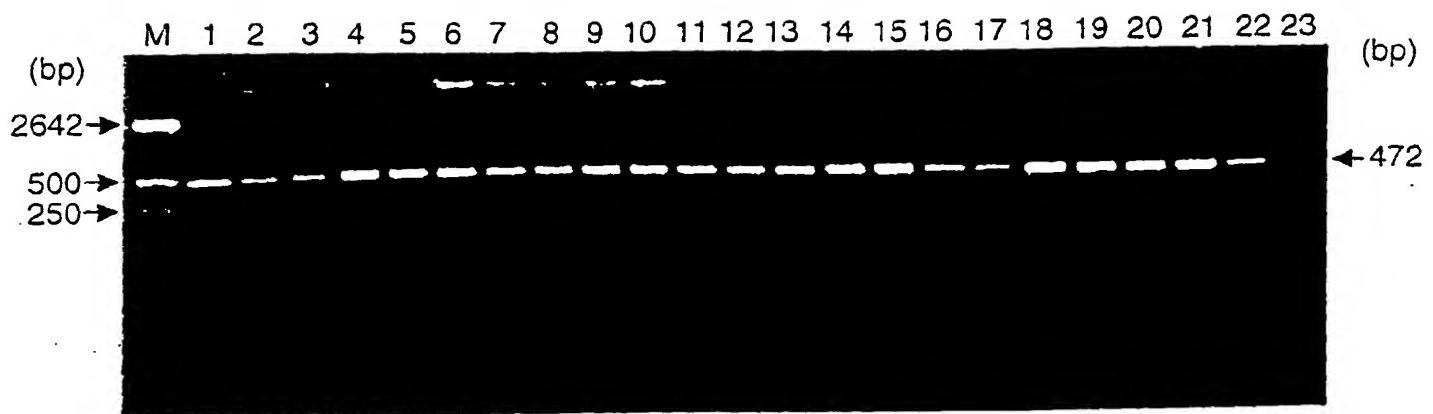
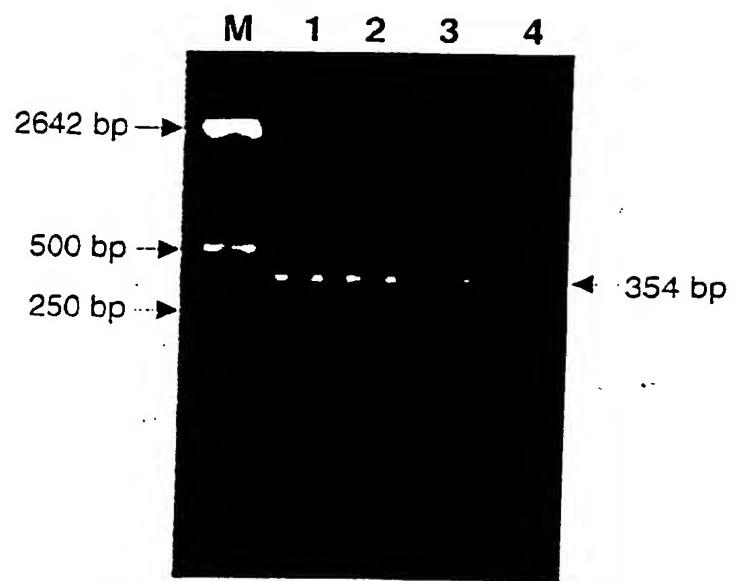


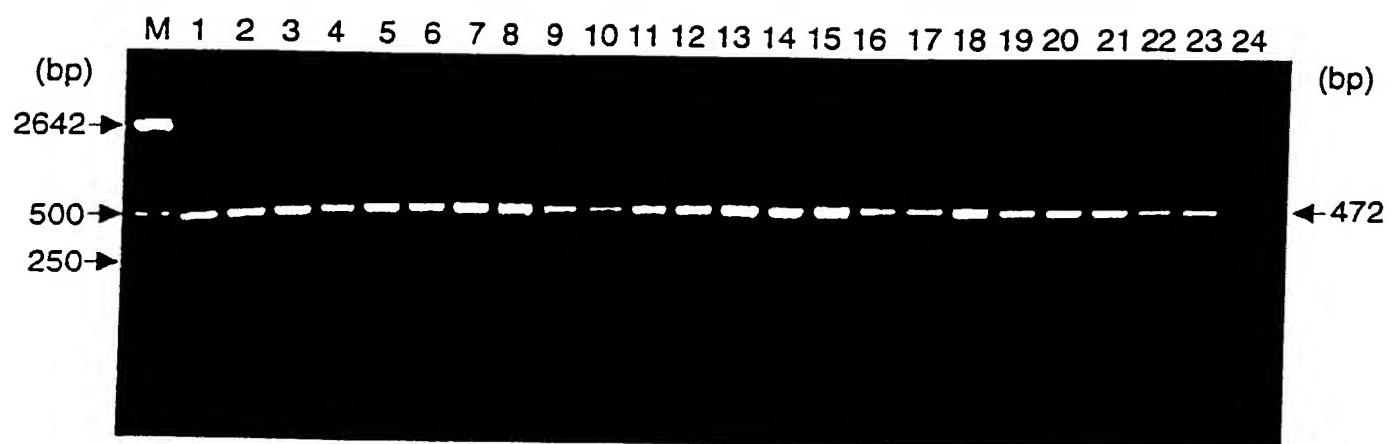
Figure 2

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**Figure 3**

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**Figure 4**

## INTERNATIONAL SEARCH REPORT

Inte Application No  
PC 1/1IV 01/00055

A. CLASSIFICATION OF SUBJECT MATTER  
IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)  
IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, EPO-Internal, EMBL, WPI Data, PAJ, MEDLINE, EMBASE

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	KOCHER T D ET AL: "DYNAMICS OF MITOCHONDRIAL DNA EVOLUTION IN ANIMALS AMPLIFICATION AND SEQUENCING WITH CONSERVED PRIMERS" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES, vol. 86, no. 16, 1989, pages 6196-6200, XP002189444 1989 ISSN: 0027-8424 the whole document ---	1-16
Y	WO 92 05277 A (DAVIDSON WILLIAM SCOTT ;BARTLETT SYLVIA ERNESTINE (CA)) 2 April 1992 (1992-04-02) the whole document ---	1-16 -/-

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

° Special categories of cited documents :

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- \*Y\* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- \*&\* document member of the same patent family

Date of the actual completion of the international search

28 February 2002

Date of mailing of the international search report

12/03/2002

Name and mailing address of the ISA  
European Patent Office, P.B. 5818 Patentlaan 2  
NL - 2280 HV Rijswijk  
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,  
Fax: (+31-70) 340-3016

Authorized officer

Hagenmaier, S

## INTERNATIONAL SEARCH REPORT

Inte  
al Application No  
PCT/IN 01/00055

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	IRWIN D M ET AL: "EVOLUTION OF THE CYTOCHROME BETA GENE OF MAMMALS" JOURNAL OF MOLECULAR EVOLUTION, SPRINGER VERLAG, NEW YORK, NY, US, vol. 2, no. 3, June 1995 (1995-06), pages 128-144, XP000892117 ISSN: 0022-2844 the whole document ---	1-16
Y	DATABASE EMBL 'Online! ID/AC AAF56513, 28 November 2000 (2000-11-28) ZH NIPPON KAGAKU SENI KENSA KYOKAI: "Animal fibre identification PCR primer #3" XP002191314 abstract ---	1-16
Y	WO 93 15215 A (HYDROCARBON RESEARCH INC) 5 August 1993 (1993-08-05) the whole document ---	1-16
Y	EP 0 807 690 A (KARL SCHMITZ SCHOLL FONDS FUER) 19 November 1997 (1997-11-19) the whole document ---	1-16
Y	MATTHEE CONRAD A ET AL: "Cytochrome b phylogeny of the family Bovidae: Resolution within the Alcelaphini, Antilopini, Neotragini, and Tragelaphini." MOLECULAR PHYLOGENETICS AND EVOLUTION, vol. 12, no. 1, June 1999 (1999-06), pages 31-46, XP001053239 ISSN: 1055-7903 the whole document ---	1-16
Y	SHANKARANARAYANAN PATTABHIRAMAN ET AL: "Mitochondrial DNA sequence divergence among big cats and their hybrids." CURRENT SCIENCE (BANGALORE), vol. 75, no. 9, 10 November 1998 (1998-11-10), pages 919-923, XP001063942 ISSN: 0011-3891 the whole document ---	1-16
A	THOMPSON JULIE D ET AL: "A comprehensive comparison of multiple sequence alignment programs." NUCLEIC ACIDS RESEARCH, vol. 27, no. 13, 1 July 1999 (1999-07-01), pages 2682-2690, XP002191669 ISSN: 0305-1048 the whole document -----	

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Information on patent family members

Int	Application No
PCT/US	01/00055

Patent document cited in search report	Publication date		Patent family member(s)	Publication date
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